

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 23.793 Seconds  
(without alignments)  
1690.542 Million cell updates/sec

Title: US-10-624-932-2\_COPY\_495\_598  
Perfect score: 559  
Sequence: 1 TSNMTYGTTFNFLGGRLMIPN.....CGEPSPDSWSLRLKKQSCEG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:  
1: geneseqp1980s:  
2: geneseqp1990s:  
3: geneseqp2000s:  
4: geneseqp2001s:  
5: geneseqp2002s:  
6: geneseqp2003as:  
7: geneseqp2003bs:  
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	559	100.0	437	4	AAB50690	Aab50690 Human HS1
2	559	100.0	544	7	ADG42581	Adg42581 Human tra
3	559	100.0	817	8	ADH71624	Adh71624 Human pro
4	559	100.0	833	8	ADH71622	Adh71622 Human pro
5	559	100.0	842	5	AAU74818	Aau74818 Human REP
6	559	100.0	842	8	ADL06574	Adl06574 Human tum
7	559	100.0	898	5	AAU85403	Aau85403 Human pro
8	559	100.0	898	5	AAU97899	Aau97899 Human net
9	559	100.0	898	8	ADH71618	Adh71618 Human pro

10	559	100.0	898	8	ADH71626	Adh71626 Human pro
11	559	100.0	899	5	AAU79939	Aau79939 Human UNC
12	559	100.0	899	7	ADG42569	Adg42569 Novel hum
13	559	100.0	899	8	ADH71636	Adh71636 Human pro
14	559	100.0	899	8	ADH71642	Adh71642 Human pro
15	559	100.0	899	8	ADH71648	Adh71648 Human pro
16	559	100.0	899	8	ADH71610	Adh71610 Human pro
17	559	100.0	899	8	ADH71628	Adh71628 Human pro
18	559	100.0	899	8	ADH71640	Adh71640 Human pro
19	559	100.0	899	8	ADH71630	Adh71630 Human pro
20	559	100.0	899	8	ADH71650	Adh71650 Human pro
21	559	100.0	899	8	ADH71644	Adh71644 Human pro
22	559	100.0	899	8	ADH71646	Adh71646 Human pro
23	559	100.0	899	8	ADH71638	Adh71638 Human pro
24	555	99.3	436	4	AAM25589	Aam25589 Human pro
25	555	99.3	899	8	ADH71632	Adh71632 Human pro
26	554	99.1	899	8	ADH71634	Adh71634 Human pro
27	553	98.9	556	2	AAW78899	Aaw78899 Human UNC
28	553	98.9	898	2	AAW78898	Aaw78898 Rat UNC-5
29	553	98.9	898	5	AAU10543	Aau10543 Rat netri
30	553	98.9	898	5	AAU97900	Aau97900 Rat netri
31	548	98.0	898	7	ADG42580	Adg42580 Rat trans
32	544	97.3	400	7	ADN95115	Adn95115 Human LEC
33	465.5	83.3	943	4	AAM79128	Aam79128 Human pro
34	347.5	62.2	266	4	AAB50650	Aab50650 Human UNC
35	345	61.7	931	7	ADG42582	Adg42582 Mouse tra
36	337	60.3	526	4	AAB50648	Aab50648 Human UNC
37	337	60.3	931	4	AAB50691	Aab50691 Human UNC
38	337	60.3	931	7	ADE63098	Ade63098 Human Pro
39	337	60.3	931	7	ABU64297	Abu64297 Human thr
40	337	60.3	931	8	ADR99258	Adr99258 Human unc
41	337	60.3	964	8	ADR99250	Adr99250 Human 1RO
42	337	60.3	982	4	ABG11551	Abg11551 Novel hum
43	334	59.7	931	7	ADG42584	Adg42584 Human tra
44	322.5	57.7	929	7	ADG42583	Adg42583 Human tra
45	318	56.9	238	4	AAB50646	Aab50646 Human UNC

#### ALIGNMENTS

RESULT 1  
AAB50690  
ID AAB50690 standard; protein; 437 AA.  
XX  
AC AAB50690;  
XX  
DT 19-MAR-2001 (first entry)  
XX  
DE Human HS1 protein SEQ ID NO:89.  
XX  
KW Human; *Caenorhabditis elegans*; UNC-5; splice variant; nematode worm;  
KW protein-protein interaction; identification.  
XX  
OS Homo sapiens.  
XX  
PN WO200073328-A2.

XX  
PD 07-DEC-2000.  
XX  
PF 02-JUN-2000; 2000WO-EP005108.  
XX  
PR 01-JUN-1999; 99GB-00012755.  
XX  
PA (DEVG-) DEVGEN NV.  
XX  
PI Van Crieckinge W, Roelens I, Bogaert T, Verwaerde P;  
XX  
DR WPI; 2001-016508/02.  
XX  
PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a  
PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for  
PT identifying unknown human cDNAs which encode proteins that interact with  
PT the human unc-5C protein.  
XX  
PS Disclosure; Page 223-224; 246pp; English.  
XX  
CC The present invention describes 3 variants of human unc-5C cDNAs (unc-  
CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-  
CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the  
CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on  
CC protein-protein-interactions between the unc-5 protein and a variety of  
CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1  
CC cDNA are useful in methods for identifying compounds which reduce or  
CC inhibit the lethal phenotype associated with the expression of the unc-5  
CC death domain in yeast. They are also useful in yeast two hybrid  
CC experiments for identifying unknown human cDNAs which encode proteins  
CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and  
CC AAB50646 to AAB50693 represent sequences used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 437 AA;

Query Match 100.0%; Score 559; DB 4; Length 437;  
Best Local Similarity 100.0%; Pred. No. 1.2e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TSNMTYGTNFLLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
Db 34 TSNMTYGTNFLLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 93  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
Db 94 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 137

RESULT 2  
ADG42581  
ID ADG42581 standard; protein; 544 AA.  
XX  
AC ADG42581;  
XX  
DT 26-FEB-2004 (first entry)  
XX

DE Human transmembrane receptor Unc5H1 homologue.  
XX  
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;  
KW NOVX-associated disorder; cancer; human; transmembrane receptor;  
KW Unc5H1 homologue.  
XX  
OS Homo sapiens.  
XX  
PN US2003204052-A1.  
XX  
PD 30-OCT-2003.  
XX  
PF 04-OCT-2001; 2001US-00970944.  
XX  
PR 04-OCT-2000; 2000US-0237862P.  
XX  
PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
XX  
PI Herrmann JL, Rastelli L, Shimkets RA;  
XX  
DR WPI; 2003-900673/82.  
XX  
PT New NOVX gene or NOVX-specific antibody, useful for preparing a  
PT composition for treating or preventing a NOVX-associated disorder, e.g.,  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 14; 118pp; English.  
XX  
CC The invention describes a new isolated polypeptide comprising: a  
CC polypeptide or its mature form comprising a sequence not given in the  
CC specification; or a variant of (A), where one or more amino acid residues  
CC in the variant differs in no more than 15% from the amino acid sequence  
CC of the mature form. The pharmaceutical composition may be administered  
CC via oral, transdermal, rectal or parenteral route. The polypeptide,  
CC nucleic acid or antibody is useful for preparing a composition for  
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is  
CC the amino acid sequence of a transmembrane receptor homologue used in a  
CC comparison with the novel human proteins of the invention.  
XX  
SQ Sequence 544 AA;

Query Match 100.0%; Score 559; DB 7; Length 544;  
Best Local Similarity 100.0%; Pred. No. 1.6e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TSNMTYGTNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 141 TSNMTYGTNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 200  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 201 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 244

RESULT 3

ADH71624  
ID ADH71624 standard; protein; 817 AA.  
XX  
AC ADH71624;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21h SEQ ID NO:520.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.  
XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.  
PR 10-JUN-2002; 2002US-0387535P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.  
PR 13-AUG-2002; 2002US-0403531P.  
PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.  
PR 15-AUG-2002; 2002US-0406317P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.  
PR 05-NOV-2002; 2002US-00423798.  
PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71623.

XX  
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.  
XX  
PS Example 21; SEQ ID NO 520; 1880pp; English.  
XX  
CC The invention relates to a novel isolated polypeptide (NOVX). A  
CC polypeptide of the invention has cytostatic, immunomodulator,  
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
CC antilipaemic activity, and may have a use in gene therapy, and as a  
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
CC any of the 303 fully defined nucleotide sequences given in the  
CC specification. The polypeptide is useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease. The  
CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
CC further used as hybridisation probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. The present sequence  
CC represents a NOVX polypeptide of the invention.  
XX  
SQ Sequence 817 AA;

Query Match 100.0%; Score 559; DB 8; Length 817;  
Best Local Similarity 100.0%; Pred. No. 2.7e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| |||||||  
Db 414 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 473  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| |||||||  
Db 474 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 517

RESULT 4  
ADH71622  
ID ADH71622 standard; protein; 833 AA.  
XX  
AC ADH71622;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21g SEQ ID NO:518.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.

XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.  
XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.  
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PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.

PR 13-AUG-2002; 2002US-0403531P.  
PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.  
PR 05-NOV-2002; 2002US-00423798.  
PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71621.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 518; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A  
CC polypeptide of the invention has cytostatic, immunomodulator,  
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
CC antilipaemic activity, and may have a use in gene therapy, and as a  
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
CC any of the 303 fully defined nucleotide sequences given in the  
CC specification. The polypeptide is useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease. The  
CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious



XX  
PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;  
PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;  
PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;  
PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;  
XX  
DR WPI; 2002-090432/12.  
DR N-PSDB; ABK15169.  
XX  
PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in  
PT the diagnosis, treatment and prevention of gastrointestinal (e.g.  
PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell  
PT proliferative (e.g. cancer) disorders.  
XX  
PS Claim 45; Page 111-113; 157pp; English.  
XX  
CC This invention relates to twelve human receptors cDNA sequences referred  
CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The  
CC proteins of the invention may have antiinflammatory, cytostatic,  
CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active  
CC general, anticonvulsant, nootropic, neuroprotective, antiallergic  
CC activities. The sequences of the invention may be used to produce REPTR  
CC agonists or antagonists, and the protein sequences may be used to raise  
CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and  
CC polypeptides of the invention are useful in the diagnosis, treatment and  
CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,  
CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine  
(e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory  
CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,  
CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,  
CC systemic lupus erythematosus), cell proliferative (e.g. cancer),  
CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological  
(e.g. epilepsy, Alzheimer's disease, Huntington's disease) and  
CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other  
CC examples of each disorder are given in the specification. The present  
CC sequence represents the human REPTR1 protein sequence of the invention  
XX  
SO Sequence 842 AA:

RESULT 6  
ADL06574  
ID ADL06574 standard; protein; 842 AA.  
XX  
AC ADL06574;

XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human tumour-associated antigenic target (TAT) polypeptide #73.  
XX  
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;  
KW cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016225-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 19-AUG-2003; 2003WO-US025892.  
XX  
PR 19-AUG-2002; 2002US-0404809P.  
PR 21-AUG-2002; 2002US-0405645P.  
PR 23-SEP-2002; 2002US-0413192P.  
PR 15-OCT-2002; 2002US-0419008P.  
PR 15-NOV-2002; 2002US-0426847P.  
PR 02-JUL-2003; 2003US-0484959P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;  
PI Spencer SD, Wu TD, Zhang Z;  
XX  
DR WPI; 2004-257144/24.  
DR N-PSDB; ADL06497.  
XX  
PT New antibody that binds to a tumor-associated antigenic target (TAT)  
PT polypeptide, useful for preparing a composition for diagnosing or  
PT treating cancer.  
XX  
PS Claim 2; SEQ ID NO 154; 319pp; English.  
XX  
CC The present invention relates to the isolation of human tumour-associated  
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also  
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is  
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a  
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is  
CC produced in bacteria or in CHO cells and induces death of a cell to which  
CC it binds. The antibody is useful for preparing a composition for  
CC diagnosing or treating tumours and cancer. The present sequence  
CC represents a human TAT polypeptide of the invention.

XX  
SQ Sequence 842 AA;

Query Match 100.0%; Score 559; DB 8; Length 842;  
Best Local Similarity 100.0%; Pred. No. 2.8e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
Db 439 TSNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 498

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPS PDSW SLRLKKQSCEG 104  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 499 LSPIVSCGPPGVLLTRPVILAMDHCGEPS PDSW SLRLKKQSCEG 542

RESULT 7  
AAU85403  
ID AAU85403 standard; protein; 898 AA.  
XX  
AC AAU85403;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human protein NOV1.  
XX  
KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;  
KW cell signal processing disorder; metabolic disorder; obesity; infection;  
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; immune disorder;  
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;  
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;  
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;  
KW psychosis; neurological disorder; anxiety; schizophrenia;  
KW manic depression; dementia; dyskinesia; Huntington's disease;  
KW Gilles de la Tourette's syndrome; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200210216-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 30-JUL-2001; 2001WO-US024225.  
XX  
PR 28-JUL-2000; 2000US-0221409P.  
PR 04-AUG-2000; 2000US-0222840P.  
PR 04-AUG-2000; 2000US-0223752P.  
PR 04-AUG-2000; 2000US-0223762P.  
PR 04-AUG-2000; 2000US-0223769P.  
PR 04-AUG-2000; 2000US-0223770P.  
PR 14-AUG-2000; 2000US-0225146P.  
PR 15-AUG-2000; 2000US-0225392P.  
PR 15-AUG-2000; 2000US-0225470P.  
PR 16-AUG-2000; 2000US-0225697P.  
PR 01-FEB-2001; 2001US-0263662P.  
PR 05-APR-2001; 2001US-0281645P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;  
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;  
XX  
DR WPI; 2002-180074/23.  
DR N-PSDB; ABK37922.  
XX  
PT New isolated cytoplasmic, nuclear, membrane bound, or secreted  
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,

PT infections, cancer, neurodegenerative, metabolic, hematopoietic and  
PT immune disorders.

xx

PS Claim 1; Page 11; 213pp; English.

xx

The invention relates to an isolated cytoplasmic, nuclear, membrane bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature form. Also included are the nucleic acids encoding the NOVX proteins, a vector comprising the nucleic acid, a cell comprising the vector, an anti-NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the antibody are useful for treating or preventing a NOVX-associated disorder, where the disorder is selected from cardiomyopathy, atherosclerosis, diabetes, a disorder related to cell signal processing and metabolic pathway modulation, metabolic disorders, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases, bacterial, fungal, protozoal and viral infections, pain, bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina pectoris, myocardial infarction, ulcer, allergy, benign prostatic hypertrophy, and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, and dyskinesias, such as Huntington's disease and Gilles de la Tourette's syndrome. The nucleic acid is useful in gene therapy. The present sequence represents a NOVX protein

xx

SQ Sequence 898 AA;

Query Match 100.0%; Score 559; DB 5; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLLMIPNTGISLLIIPPDAI PRGKIEIYLTLLHKPEDVRLPLAGCQTL 60  
|||||

Db 495 TSNMTYGTFNFLGGRLMI PNTGISLLIPPDALI PRGKIEIYLTLHKPEDVRLPLAGCQTL 554

Qy 61 LSPIVSCGPPGVLLTRPVIAMDHCGEPSPDSSWSLRLKKQSCEG 104

For more information about the study, please contact Dr. John Smith at (555) 123-4567 or via email at [john.smith@researchinstitute.org](mailto:john.smith@researchinstitute.org).

**D<sub>b</sub>** 555 LSPIVSCGPPGVLLTRPVI LAMDHC GEPS PDSW SRLKK QSEG 598

## RESULT 8

AAU97899

ID AAU97899 standard; protein; 898 AA.

xx

AC AAU97899;

xx

DT 27-AUG-2002 (first entry)

xx

## Human netrin binding membrane receptor UNC5H-1 protein.

144

KW Netrin binding membrane receptor; receptor; UNC5H-1; human; neurotropic;  
KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;  
KW central nervous system; CNS; stroke; Parkinson's disease;

KW multiple sclerosis; Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Domain 152. .223  
FT /note= "Immunoglobulin domain "  
FT Domain 247. .294  
FT /note= "Thrombospondine type 1 domain "  
FT Domain 302. .348  
FT /note= "Thrombospondine type 1 domain"  
FT Region 361. .382  
FT /note= "Transmembrane region"  
FT Domain 495. .598  
FT /note= "ZU5 domain"  
FT Domain 817. .897  
FT /note= "Death domain"  
XX  
PN WO200233080-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 15-OCT-2001; 2001WO-EP011891.  
XX  
PR 16-OCT-2000; 2000US-0240061P.  
XX  
PA (FARB ) BAYER AG.  
XX  
PI Koehler RH;  
XX  
DR WPI; 2002-463314/49.  
DR N-PSDB; ABK52891.  
XX  
PT Novel human netrin binding membrane receptor polypeptide and  
PT polynucleotides for identifying modulating agents useful in treating  
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,  
PT Alzheimer's disease.  
XX  
PS Claim 1; Fig 2; 94pp; English.  
XX  
CC This invention relates to the DNA and protein sequences of a novel  
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA  
CC sequence of the invention is useful as a probe for detecting a nucleic  
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences  
CC of the invention are useful to screen for agents which decrease the  
CC activity of the UNC5H-1 protein. The sequences are also useful for  
CC screening agents which regulate (modulate) the activity of the protein of the  
CC invention. A pharmaceutical composition containing the protein of the  
CC invention or a reagent that modulates the activity of the UNC5H-1 protein  
CC may be useful for treating a UNC5H-1 dysfunction related disease such as  
CC cancer or a central nervous system (CNS) disorders (e.g., Parkinson's  
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion  
CC proteins comprising the UNC5H-1 protein are useful for generating  
CC antibodies and for in various assay systems, and the protein can be used  
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method  
CC of the invention is useful for detecting a coding sequence for the UNC5H-  
CC 1 protein. The present sequence represents the human netrin binding

CC membrane receptor UNC5H-1 protein of the invention  
XX  
SQ Sequence 898 AA;

Query Match 100.0%; Score 559; DB 5; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 495 TSNMTYGTNFNLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 554

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 9  
ADH71618  
ID ADH71618 standard; protein; 898 AA.  
XX  
AC ADH71618;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21e SEQ ID NO:514.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.  
XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.  
PR 13-AUG-2002; 2002US-0403531P.  
PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.  
PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71617.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 514; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A  
CC polypeptide of the invention has cytostatic, immunomodulator,  
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
CC antilipaemic activity, and may have a use in gene therapy, and as a  
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
CC any of the 303 fully defined nucleotide sequences given in the  
CC specification. The polypeptide is useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease. The  
CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
CC further used as hybridisation probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. The present sequence  
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 898 AA;

Query Match 100.08; Score 559; DB 8; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 495 TSNMTYGTFNFLGGRLMIPNTGISLLIPPAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 10

ADH71626  
ID ADH71626 standard; protein; 898 AA.  
XX  
AC ADH71626;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21i SEQ ID NO:522.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.  
XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.  
PR 10-JUN-2002; 2002US-0387535P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.  
PR 13-AUG-2002; 2002US-0403531P.  
PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.  
PR 15-AUG-2002; 2002US-0406317P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.  
PR 05-NOV-2002; 2002US-00423798.  
PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Günther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71625.

XX  
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX  
PS Example 21; SEQ ID NO 522; 1880pp; English.  
XX

CC The invention relates to a novel isolated polypeptide (NOVX). A  
CC polypeptide of the invention has cytostatic, immunomodulator,  
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
CC antilipaemic activity, and may have a use in gene therapy, and as a  
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
CC any of the 303 fully defined nucleotide sequences given in the  
CC specification. The polypeptide is useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease. The  
CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
CC further used as hybridisation probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. The present sequence  
CC represents a NOVX polypeptide of the invention.

XX  
SQ Sequence 898 AA;

Query Match 100.0%; Score 559; DB 8; Length 898;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 494 TSNMTYGTNFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 553

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 554 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 597

RESULT 11

AAU79939

ID AAU79939 standard; protein; 899 AA.

XX  
AC AAU79939;

XX  
DT 15-JUL-2002 (first entry)

XX  
DE Human UNC5-like protein NOV1.

XX  
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;  
KW cell signal processing; metabolic pathway modulation; cancerous tissue;  
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;  
KW chromosome 13.

XX  
OS Homo sapiens.

XX  
PN WO200229038-A2.

XX

PD 11-APR-2002.  
XX  
PF 04-OCT-2001; 2001WO-US031377.  
XX  
PR 04-OCT-2000; 2000US-0237862P.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Herrmann JL, Rastelli L, Shimkets RA;  
XX  
DR WPI; 2002-340104/37.  
DR N-PSDB; ABK49422.  
XX  
PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for  
PT treating cardiomyopathy, atherosclerosis, and cancer.  
XX  
PS Claim 1; Page 9; 180pp; English.  
XX  
CC The present invention relates to a new NOVX polypeptide having a 900  
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)  
CC residue amino acid sequence, as given in the specification. The novel  
CC polypeptide, and its encoding polynucleotide, are used to treat  
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell  
CC signal processing and metabolic pathway modulation, in a human. Detecting  
CC the polypeptide or polynucleotide is useful for identifying cancerous  
CC tissue. The antibody can be used to treat diabetes or cancer. The host  
CC cells can be used to produce non-human transgenic animals useful in drug  
CC screening. The present amino acid sequence is that of the human UNC5-like  
CC protein NOV1 of the invention. This sequence is encoded by the human UNC5  
CC -like NOV1 gene located on chromosome 13  
XX  
SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 5; Length 899;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| |||||||  
Db 495 TSNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| |||||||  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 12  
ADG42569  
ID ADG42569 standard; protein; 899 AA.  
XX  
AC ADG42569;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Novel human NOV1.  
XX  
KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;

KW NOVX-associated disorder; cancer; human.  
XX  
OS Homo sapiens.  
XX  
PN US2003204052-A1.  
XX  
PD 30-OCT-2003.  
XX  
PF 04-OCT-2001; 2001US-00970944.  
XX  
PR 04-OCT-2000; 2000US-0237862P.  
XX  
PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
XX  
PI Herrmann JL, Rastelli L, Shimkets RA;  
XX  
DR WPI; 2003-900673/82.  
DR N-PSDB; ADG42568.  
XX  
PT New NOVX gene or NOVX-specific antibody, useful for preparing a  
PT composition for treating or preventing a NOVX-associated disorder, e.g.,  
PT cancer.  
XX  
PS Claim 1; SEQ ID NO 2; 118pp; English.  
XX  
CC The invention describes a new isolated polypeptide comprising: a  
CC polypeptide or its mature form comprising a sequence not given in the  
CC specification; or a variant of (A), where one or more amino acid residues  
CC in the variant differs in no more than 15% from the amino acid sequence  
CC of the mature form. The pharmaceutical composition may be administered  
CC via oral, transdermal, rectal or parenteral route. The polypeptide,  
CC nucleic acid or antibody is useful for preparing a composition for  
CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is  
CC the amino acid sequence of a human NOVX protein.  
XX  
SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 7; Length 899;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| |||||||  
Db 495 TSNMTYGTNFNLGGRLMIPNTGISLLIIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
| |||||||  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDSDSLRLKKQSCEG 104  
| |||||||  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDSDSLRLKKQSCEG 598

RESULT 13  
ADH71636  
ID ADH71636 standard; protein; 899 AA.  
XX  
AC ADH71636;

XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21n SEQ ID NO:532.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.  
XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.  
PR 10-JUN-2002; 2002US-0387535P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.  
PR 13-AUG-2002; 2002US-0403531P.  
PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.  
PR 05-NOV-2002; 2002US-00423798.  
PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71635.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX  
PS Example 21; SEQ ID NO 532; 1880pp; English.  
XX  
CC The invention relates to a novel isolated polypeptide (NOVX). A  
CC polypeptide of the invention has cytostatic, immunomodulator,  
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
CC antilipaemic activity, and may have a use in gene therapy, and as a  
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
CC any of the 303 fully defined nucleotide sequences given in the  
CC specification. The polypeptide is useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease. The  
CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
CC further used as hybridisation probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. The present sequence  
CC represents a NOVX polypeptide of the invention.

XX  
SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 8; Length 899;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 TSNMTYGTNFLLGGRLMIPNTGISLLIPPAI PRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| |||||||  
Db 495 TSNMTYGTNFLLGGRLMIPNTGISLLIPPAI PRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| |||||||  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 14  
ADH71642  
ID ADH71642 standard; protein; 899 AA.  
XX  
AC ADH71642;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21q SEQ ID NO:538.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.

XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.  
PR 10-JUN-2002; 2002US-0387535P.  
PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.  
PR 13-AUG-2002; 2002US-0403531P.  
PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.  
PR 05-NOV-2002; 2002US-00423798.  
PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;  
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Paturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71641.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 538; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A  
CC polypeptide of the invention has cytostatic, immunomodulator,  
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and  
CC antilipaemic activity, and may have a use in gene therapy, and as a  
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising  
CC any of the 303 fully defined nucleotide sequences given in the  
CC specification. The polypeptide is useful in the manufacture of a  
CC medicament for treating a syndrome associated with a human disease. The  
CC polypeptide, polynucleotide and antibody are useful in diagnosing,  
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,  
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious  
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are  
CC further used as hybridisation probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. The present sequence  
CC represents a NOVX polypeptide of the invention.

XX  
SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 8; Length 899;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| |||||||  
Db 495 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 554

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| |||||||  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 15  
ADH71648  
ID ADH71648 standard; protein; 899 AA.  
XX  
AC ADH71648;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Human protein of the invention NOV21t SEQ ID NO:544.  
XX  
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;  
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;  
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;  
KW obesity; diabetes; infectious disease; metabolic syndrome X;  
KW dyslipidaemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2003102155-A2.  
XX  
PD 11-DEC-2003.  
XX  
PF 03-JUN-2003; 2003WO-US017430.  
XX  
PR 03-JUN-2002; 2002US-0385120P.  
PR 04-JUN-2002; 2002US-0385784P.  
PR 05-JUN-2002; 2002US-0386041P.  
PR 05-JUN-2002; 2002US-0386047P.  
PR 06-JUN-2002; 2002US-0386376P.  
PR 06-JUN-2002; 2002US-0386453P.  
PR 06-JUN-2002; 2002US-0386864P.  
PR 06-JUN-2002; 2002US-0387016P.  
PR 07-JUN-2002; 2002US-0386796P.  
PR 07-JUN-2002; 2002US-0386816P.  
PR 07-JUN-2002; 2002US-0386931P.  
PR 07-JUN-2002; 2002US-0386942P.  
PR 07-JUN-2002; 2002US-0386971P.  
PR 07-JUN-2002; 2002US-0387262P.  
PR 08-JUN-2002; 2002US-0296960P.  
PR 10-JUN-2002; 2002US-0387400P.  
PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.  
PR 11-JUN-2002; 2002US-0387625P.  
PR 11-JUN-2002; 2002US-0387634P.  
PR 11-JUN-2002; 2002US-0387668P.  
PR 11-JUN-2002; 2002US-0387696P.  
PR 11-JUN-2002; 2002US-0387702P.  
PR 11-JUN-2002; 2002US-0387836P.  
PR 11-JUN-2002; 2002US-0387859P.  
PR 12-JUN-2002; 2002US-0387933P.  
PR 12-JUN-2002; 2002US-0387934P.  
PR 12-JUN-2002; 2002US-0387960P.  
PR 12-JUN-2002; 2002US-0388022P.  
PR 12-JUN-2002; 2002US-0388096P.  
PR 13-JUN-2002; 2002US-0389123P.  
PR 14-JUN-2002; 2002US-0389118P.  
PR 14-JUN-2002; 2002US-0389120P.  
PR 14-JUN-2002; 2002US-0389144P.  
PR 14-JUN-2002; 2002US-0389146P.  
PR 17-JUN-2002; 2002US-0389729P.  
PR 17-JUN-2002; 2002US-0389742P.  
PR 18-JUN-2002; 2002US-0389884P.  
PR 19-JUN-2002; 2002US-0390006P.  
PR 19-JUN-2002; 2002US-0390209P.  
PR 21-JUN-2002; 2002US-0390763P.  
PR 17-JUL-2002; 2002US-0396706P.  
PR 06-AUG-2002; 2002US-0401628P.  
PR 09-AUG-2002; 2002US-0402156P.  
PR 09-AUG-2002; 2002US-0402256P.  
PR 09-AUG-2002; 2002US-0402389P.  
PR 12-AUG-2002; 2002US-0402786P.  
PR 12-AUG-2002; 2002US-0402816P.  
PR 12-AUG-2002; 2002US-0402821P.  
PR 12-AUG-2002; 2002US-0402832P.  
PR 13-AUG-2002; 2002US-0403448P.  
PR 13-AUG-2002; 2002US-0403459P.  
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PR 13-AUG-2002; 2002US-0403532P.  
PR 13-AUG-2002; 2002US-0403563P.  
PR 13-AUG-2002; 2002US-0406317P.  
PR 15-AUG-2002; 2002US-0403617P.  
PR 26-AUG-2002; 2002US-0406182P.  
PR 26-AUG-2002; 2002US-0406355P.  
PR 27-AUG-2002; 2002US-0406240P.  
PR 12-SEP-2002; 2002US-0410084P.  
PR 20-SEP-2002; 2002US-0412528P.  
PR 23-SEP-2002; 2002US-0412731P.  
PR 30-SEP-2002; 2002US-0414801P.  
PR 30-SEP-2002; 2002US-0414839P.  
PR 30-SEP-2002; 2002US-0414840P.  
PR 30-SEP-2002; 2002US-0414954P.  
PR 09-OCT-2002; 2002US-0417186P.  
PR 09-OCT-2002; 2002US-0417406P.  
PR 23-OCT-2002; 2002US-0420639P.  
PR 28-OCT-2002; 2002US-0421156P.  
PR 31-OCT-2002; 2002US-0422690P.  
PR 01-NOV-2002; 2002US-0423130P.  
PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.  
PR 12-NOV-2002; 2002US-0425453P.

xx

PA

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PI

PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;  
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;  
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;  
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;  
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;  
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;  
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;  
PI Zhong H;

xx

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71647.

xx

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or  
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

xx

PS Example 21; SEQ ID NO 544; 1880pp; English.

xx

The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and antilipidaemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence represents a NOVX polypeptide of the invention.

xx

SQ Sequence 899 AA;

Query Match 100.0%; Score 559; DB 8; Length 899;  
Best Local Similarity 100.0%; Pred. No. 3e-57;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIIPPDAI PRGKIEIYLTLHKPEDVRLPLAGCQLT 60  
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Qy 61 LSPIVSCGPPGVLLTRPVLAMDHCGEPSQDSWSLRLKKQSCEG 104  
|||||

Search completed: March 1, 2005, 08:56:49

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:42:47 ; Search time 6.2315 Seconds  
(without alignments)  
1245.848 Million cell updates/sec

Title: US-10-624-932-2\_COPY\_495\_598  
Perfect score: 559  
Sequence: 1 TSNMTYGTFNFLGGRLMIPN.....CGEPSPDSWSLRKKQSCEG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	553	98.9	557	2	US-08-808-982-6 Sequence 6, Appli
2	553	98.9	557	3	US-09-306-902A-6 Sequence 6, Appli
3	553	98.9	898	2	US-08-808-982-5 Sequence 5, Appli
4	553	98.9	898	3	US-09-306-902A-5 Sequence 5, Appli
5	337	60.3	769	4	US-09-949-016-10665 Sequence 10665, A
6	277	49.6	943	2	US-08-808-982-7 Sequence 7, Appli
7	277	49.6	943	3	US-09-306-902A-7 Sequence 7, Appli
8	243.5	43.6	655	4	US-09-969-532-32 Sequence 32, Appli
9	243.5	43.6	666	4	US-09-969-532-30 Sequence 30, Appli
10	243.5	43.6	669	4	US-09-969-532-28 Sequence 28, Appli
11	243.5	43.6	680	4	US-09-969-532-26 Sequence 26, Appli

12	243.5	43.6	886	4	US-09-969-532-16	Sequence 16, Appl
13	243.5	43.6	897	4	US-09-969-532-14	Sequence 14, Appl
14	243.5	43.6	900	4	US-09-969-532-12	Sequence 12, Appl
15	243.5	43.6	911	4	US-09-969-532-10	Sequence 10, Appl
16	163.5	29.2	1736	4	US-09-919-497-98	Sequence 98, Appl
17	163.5	29.2	1771	4	US-09-949-016-9470	Sequence 9470, Ap
18	139.5	25.0	251	4	US-09-270-767-45766	Sequence 45766, A
19	132.5	23.7	321	4	US-09-969-532-24	Sequence 24, Appl
20	132.5	23.7	332	4	US-09-969-532-22	Sequence 22, Appl
21	132.5	23.7	335	4	US-09-969-532-20	Sequence 20, Appl
22	132.5	23.7	346	4	US-09-969-532-18	Sequence 18, Appl
23	132.5	23.7	552	4	US-09-969-532-8	Sequence 8, Appli
24	132.5	23.7	563	4	US-09-969-532-6	Sequence 6, Appli
25	132.5	23.7	566	4	US-09-969-532-4	Sequence 4, Appli
26	132.5	23.7	577	4	US-09-969-532-2	Sequence 2, Appli
27	80.5	14.4	85	4	US-09-270-767-41828	Sequence 41828, A
28	76	13.6	147	4	US-09-270-767-61289	Sequence 61289, A
29	72	12.9	345	4	US-09-214-631-5	Sequence 5, Appli
30	72	12.9	1719	4	US-09-949-016-6966	Sequence 6966, Ap
31	72	12.9	1856	4	US-09-949-016-6964	Sequence 6964, Ap
32	72	12.9	1880	4	US-09-949-016-5876	Sequence 5876, Ap
33	72	12.9	1881	4	US-09-949-016-6965	Sequence 6965, Ap
34	72	12.9	1883	4	US-09-949-016-9010	Sequence 9010, Ap
35	72	12.9	1883	4	US-09-949-016-9011	Sequence 9011, Ap
36	72	12.9	1883	4	US-09-949-016-9012	Sequence 9012, Ap
37	72	12.9	1883	4	US-09-949-016-9013	Sequence 9013, Ap
38	72	12.9	1883	4	US-09-949-016-9014	Sequence 9014, Ap
39	72	12.9	1883	4	US-09-949-016-9015	Sequence 9015, Ap
40	72	12.9	1883	4	US-09-949-016-9016	Sequence 9016, Ap
41	72	12.9	1883	4	US-09-949-016-9017	Sequence 9017, Ap
42	68	12.2	346	1	US-08-213-403-2	Sequence 2, Appli
43	68	12.2	346	1	US-08-458-077-2	Sequence 2, Appli
44	68	12.2	346	1	US-08-460-741-2	Sequence 2, Appli
45	68	12.2	346	1	US-08-747-240-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
 US-08-808-982-6  
 ; Sequence 6, Application US/08808982  
 ; Patent No. 5939271  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tessier-Lavigne, Marc  
 ; APPLICANT: Leonardo, E. David  
 ; APPLICANT: Hink, Lindsay  
 ; APPLICANT: Masu, Masayuki  
 ; APPLICANT: Kazuko, Keino-Masu  
 ; TITLE OF INVENTION: Netrin Receptors  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 ; STREET: 268 BUSH STREET, SUITE 3200  
 ; CITY: SAN FRANCISCO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA

; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/808,982  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide

US-08-808-982-6

Query Match 98.9%; Score 553; DB 2; Length 557;  
Best Local Similarity 99.0%; Pred. No. 1.2e-60;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPPSPDSWSLRLKKQSCEG 104  
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Db 213 LSPIVSCGPPGVLLTRPVILAMDHCGEPPSPDSWSLALKQSCEG 256

## RESULT 2

US-09-306-902A-6

; Sequence 6, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc  
; Leonardo, E. David  
; Hink, Lindsay  
; Masu, Masayuki  
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA

; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/306,902A  
; FILING DATE: 07-May-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 557 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-306-902A-6

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Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 153 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 212  
  
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Db 213 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLALKQSCEG 256

RESULT 3  
US-08-808-982-5  
; Sequence 5, Application US/08808982  
; Patent No. 5939271  
; GENERAL INFORMATION:  
; APPLICANT: Tessier-Lavigne, Marc  
; APPLICANT: Leonardo, E. David  
; APPLICANT: Hink, Lindsay  
; APPLICANT: Masu, Masayuki  
; APPLICANT: Kazuko, Keino-Masu  
; TITLE OF INVENTION: Netrin Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA

; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/808,982  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 898 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide

US-08-808-982-5

Query Match 98.9%; Score 553; DB 2; Length 898;  
Best Local Similarity 98.1%; Pred. No. 2.2e-60;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 495 TSNMAYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQL 554

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPPSPDSWSLRLKKQSCEG 104  
Db 555 LSPVVSCGPPGVLLTRPVILAMDHCGEPPSPDSWSLRLKKQSCEG 598

RESULT 4

US-09-306-902A-5

; Sequence 5, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc  
; Leonardo, E. David  
; Hink, Lindsay  
; Masu, Masayuki  
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA

;  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/306,902A  
; FILING DATE: 07-May-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 898 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-306-902A-5

Query Match 98.9%; Score 553; DB 3; Length 898;  
Best Local Similarity 98.1%; Pred. No. 2.2e-60;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 495 TSNMAYGTNFNFGGRLMIPNTGISLLIPPAI PRGK IYEIYLTLHKP EDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHC GEPS DSWSLRLKKQSCEG 104  
Db 555 LSPVVSCGPPGVLLTRPVILAMDHC GEPS DSWSLRLKKQSCEG 598

RESULT 5  
US-09-949-016-10665  
; Sequence 10665, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES  
THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10665  
; LENGTH: 769  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10665

Query Match 60.3%; Score 337; DB 4; Length 769;  
Best Local Similarity 55.6%; Pred. No. 2.1e-33;  
Matches 55; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

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Db 371 FGSFNSLGGHLIVPNNSGVSLIPAGAI PQGRVYEMYVTVHRKETMRPPMDDSQTLTGVV 430  
  
Qy 66 SCGPPGVLLTRPVILAMDHCGEPSWLSRLKKQSCEG 104  
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Db 431 SCGPPGALLTRPVVLTMHHCADPNTEDWKILLKNQAAQG 469

## RESULT 6

US-08-808-982-7

; Sequence 7, Application US/08808982  
; Patent No. 5939271  
; GENERAL INFORMATION:  
; APPLICANT: Tessier-Lavigne, Marc  
; APPLICANT: Leonardo, E. David  
; APPLICANT: Hink, Lindsay  
; APPLICANT: Masu, Masayuki  
; APPLICANT: Kazuko, Keino-Masu  
; TITLE OF INVENTION: Netrin Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/808,982  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 943 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide

US-08-808-982-7

Query Match 49.6%; Score 277; DB 2; Length 943;  
Best Local Similarity 52.9%; Pred. No. 9.1e-26;  
Matches 55; Conservative 17; Mismatches 30; Indels 2; Gaps 2;

Qy 2 SNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLA-GCQTL 60  
|: ||| ||||| || |||:|||:| |||:|| |::|| ::| | |||: | ||:  
Db 540 SSSVSGTGFGLGGRLTIPGTGVSLVPNGAIPQGKFYDLYLRINKTEST-LPLSEGSQTV 598  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 104  
||| |:||| |:||| |||:| :||| | | :||| |: :||  
Db 599 LSPSVTCGPTGLLLCPVVLTVPHCAEVIAAGDWIFQLKTQAHQG 642

RESULT 7

US-09-306-902A-7

; Sequence 7, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc  
; Leonardo, E. David  
; Hink, Lindsay  
; Masu, Masayuki  
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/306,902A  
; FILING DATE: 07-May-1999  
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 943 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-306-902A-7

Query Match 49.6%; Score 277; DB 3; Length 943;  
Best Local Similarity 52.9%; Pred. No. 9.1e-26;  
Matches 55; Conservative 17; Mismatches 30; Indels 2; Gaps 2;  
  
Qy 2 SNMTYGTFNFLGGRLMIPNTGISLLIPPDPAIPRGKIEIYLTLHKPEDVRLPLA-GCQTL 60  
|: |||| ||||| || ||::||:| ||||:|| |::|| :|| | |||: | ||:  
Db , 540 SSSVSGTFGCLGGRLTIPGTGVSLVPNGAIPQGKFYDLYLRINKTEST-LPLSEGSQTV 598  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
||| |:||| |::| | ||::| :|| | | :|| |: :|  
Db 599 LSPEVTCGPTGLLCRPVVLTVPHCAEVIAQDWIFQLKTQAHQG 642

RESULT 8

US-09-969-532-32  
; Sequence 32, Application US/09969532  
; Patent No. 6777232  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Scoville, John  
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides  
Encoding the Same  
; FILE REFERENCE: LEX-0244-USA  
; CURRENT APPLICATION NUMBER: US/09/969,532  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 60/237,280  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 655  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-969-532-32

Query Match 43.6%; Score 243.5; DB 4; Length 655;  
Best Local Similarity 45.2%; Pred. No. 8.9e-22;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;  
  
Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | |||||::|:|||:| ||| | :|||:||:| | | | :|  
Db 242 TELRTTGVFGHLGGRLVMPNTGVSLIIPHGAIPPEENSWEIYMSINQGEP-SLQSDGSEVL 300  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
||| |:||| | ::| | | :|| | :| :|||: :|  
Db 301 LSPEVTCGPPDMIVTPPFALTIPHCADVSSEHWNHLKKRTQQG 344

RESULT 9

US-09-969-532-30

; Sequence 30, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 666

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-969-532-30

Query Match 43.6%; Score 243.5; DB 4; Length 666;  
Best Local Similarity 45.2%; Pred. No. 9.1e-22;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIAPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | ||||:|||:|||| | || :|||::: | | | | : |  
Db 253 TELRTTGVFGHLGGRLVMPNTGVSLLIPHGAYPEENSWEIYMSINQGEP-SLQSDGSEVL 311

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| | | :|||: ::| | | : || : | : |:: |||:: :|  
Db 312 LSPEVTCGPPDMIVTPFALTIPHCADVSSEHWNIAHLKKRTQQG 355

RESULT 10

US-09-969-532-28

; Sequence 28, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 669

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-969-532-28

Query Match 43.6%; Score 243.5; DB 4; Length 669;  
Best Local Similarity 45.2%; Pred. No. 9.2e-22;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;  
  
Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | |||||:::||||| ||| :|||::::: | | | | : |  
Db 256 TELRTTGVFGHLGGRLVMPNTGVSLIIPHGAYPEENSWEIYMSINQGEP-SLQSDGSEVL 314  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
||| |:|||| ::::| | | : || : | : |:: |||:: :|  
Db 315 LSPEVTCGPPDMIVTPFALTIPHCADVSSEHWNIIHLKKRTQQG 358

RESULT 11

US-09-969-532-26

; Sequence 26, Application US/09969532  
; Patent No. 6777232  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Scoville, John  
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides  
Encoding the Same  
; FILE REFERENCE: LEX-0244-USA  
; CURRENT APPLICATION NUMBER: US/09/969,532  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 60/237,280  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 680  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-969-532-26

Query Match 43.6%; Score 243.5; DB 4; Length 680;  
Best Local Similarity 45.2%; Pred. No. 9.4e-22;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;  
  
Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | |||||:::||||| ||| :|||::::: | | | | : |  
Db 267 TELRTTGVFGHLGGRLVMPNTGVSLIIPHGAYPEENSWEIYMSINQGEP-SLQSDGSEVL 325  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
||| |:|||| ::::| | | : || : | : |:: |||:: :|  
Db 326 LSPEVTCGPPDMIVTPFALTIPHCADVSSEHWNIIHLKKRTQQG 369

RESULT 12.

US-09-969-532-16

; Sequence 16, Application US/09969532  
; Patent No. 6777232  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides  
Encoding the Same  
; FILE REFERENCE: LEX-0244-USA  
; CURRENT APPLICATION NUMBER: US/09/969,532  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 60/237,280  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 886  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-969-532-16

Query Match 43.6%; Score 243.5; DB 4; Length 886;  
Best Local Similarity 45.2%; Pred. No. 1.3e-21;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAlPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | |||||:::||||| ||| :|||::::: | | | | : |  
Db 473 TELRTTGVFGHLGGRLVMPNTGVSLIIPHGAPEENSWEIYMSINQGEP-SLQSDGSEVL 531

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
| | | |:|||| ::::| | | : || : | : |:: |||:: : |  
Db 532 LSPEVTCGPPDMIVTPFALTIPHCADVSSEHWNIHLKKRTQQG 575

#### RESULT 13

US-09-969-532-14

; Sequence 14, Application US/09969532  
; Patent No. 6777232  
; GENERAL INFORMATION:  
; APPLICANT: Walke, D. Wade  
; APPLICANT: Scoville, John  
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides  
Encoding the Same  
; FILE REFERENCE: LEX-0244-USA  
; CURRENT APPLICATION NUMBER: US/09/969,532  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 60/237,280  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 897  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-969-532-14

Query Match 43.6%; Score 243.5; DB 4; Length 897;  
Best Local Similarity 45.2%; Pred. No. 1.3e-21;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAlPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | |||||:::||||| ||| :|||::::: | | | | : |  
Db 484 TELRTTGVFGHLGGRLVMPNTGVSLIIPHGAPEENSWEIYMSINQGEP-SLQSDGSEVL 542



; SEQ ID NO 10  
; LENGTH: 911  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-969-532-10

Query Match 43.6%; Score 243.5; DB 4; Length 911;  
Best Local Similarity 45.2%; Pred. No. 1.4e-21;  
Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | ||||:||||:|||| | | :|||::::: | | | | : |  
Db 498 TELRTTGVFGHLGGRLVMPNTGVSSLIPHGAYPEENSWEIYMSINQGEP-SLQSDGSEVL 556

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
| | | |:|||| ::::| | | : | | : | : |:: | |:: :|  
Db 557 LSPEVTCGPPDMIVTPFALTIPHCADVSSEHWNIIHLKKRTQQG 600

Search completed: March 1, 2005, 09:05:53  
Job time : 7.2315 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 4.05992 Seconds  
(without alignments)  
2464.715 Million cell updates/sec

Title: US-10-624-932-2\_COPY\_495\_598  
Perfect score: 559  
Sequence: 1 TSNMTYGTFNFLGGRLMIPN.....CGEPSPDSWSLRLKKQSCEG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	163.5	29.2	1736	2	A47747	tight junction pro
2	162.5	29.1	1745	2	A46431	tight junction-ass
3	96	17.2	919	2	T32541	unc-5 protein - Ca
4	96	17.2	947	1	B44294	unc-5 protein, lon
5	76	13.6	346	2	S21265	acetylserotonin O-
6	73	13.1	1848	2	S37771	ankyrin, erythrocy
7	73	13.1	1862	2	I49502	ankyrin - mouse
8	72	12.9	1856	2	B35049	ankyrin 1, erythro
9	72	12.9	1880	2	A35049	ankyrin 1, erythro
10	72	12.9	1881	1	SJHUK	ankyrin 1, erythro
11	70	12.5	384	2	S73122	carbamoyl phosphat
12	69.5	12.4	369	2	D72240	tRNA guanine trans
13	69	12.3	345	2	I48780	Stral/Eplg2 protei

14	69	12.3	345	2	I58406	LERK-2 - rat
15	68	12.2	346	2	S46993	elk ligand - human
16	68	12.2	388	1	VCVGAC	coat protein - art
17	68	12.2	803	2	S76106	hypothetical prote
18	68	12.2	999	2	AG2413	hypothetical prote
19	66.5	11.9	285	2	B83883	sugar transport sy
20	66.5	11.9	544	2	C95854	probable trehalose
21	66	11.8	201	2	D82590	hypothetical prote
22	66	11.8	467	2	A60667	cysteine proteinas
23	65.5	11.7	217	2	T47175	hypothetical prote
24	65.5	11.7	235	2	G72484	hypothetical prote
25	65.5	11.7	411	2	A55610	corticotropin-rele
26	65	11.6	388	2	S24926	coat protein, 41K
27	64.5	11.5	467	2	A45629	cysteine proteinas
28	64	11.4	579	2	G75142	abc transporter, A
29	63.5	11.4	256	2	S74928	hypothetical prote
30	63.5	11.4	400	2	D83892	transcription regu
31	62.5	11.2	236	2	T40833	haloacid dehalogen
32	62.5	11.2	255	2	AD1946	hypothetical prote
33	62.5	11.2	260	2	G70568	hypothetical prote
34	62.5	11.2	363	2	B97199	uncharacterized co
35	62.5	11.2	498	1	VHIVA6	nucleoprotein - in
36	62	11.1	253	2	G72598	probable ABC trans
37	62	11.1	270	2	B83387	hypothetical prote
38	61.5	11.0	170	2	AI3322	hypothetical prote
39	61.5	11.0	434	1	DEEBHT	histidinol dehydro
40	61.5	11.0	445	2	D81716	hypothetical prote
41	61.5	11.0	710	2	D72091	type III secretion
42	61.5	11.0	710	2	C86531	low calcium respon
43	61.5	11.0	1022	2	T49683	probable oxoglutar
44	61.5	11.0	1396	2	T10627	hypothetical prote
45	61	10.9	99	2	S42360	capsicein - Phytop

## ALIGNMENTS

RESULT 1  
A47747  
tight junction protein ZO-1 - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 09-Jul-2004  
C;Accession: A47747  
R;Willott, E.; Balda, M.S.; Fanning, A.S.; Jameson, B.; Van Itallie, C.;  
Anderson, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 90, 7834-7838, 1993  
A;Title: The tight junction protein ZO-1 is homologous to the Drosophila discs-large tumor suppressor protein of septate junctions.  
A;Reference number: A47747; MUID:93361541; PMID:8395056  
A;Accession: A47747  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1736 <WIL>  
A;Cross-references: UNIPROT:Q07157; GB:L14837; NID:g292937; PIDN:AAA02891.1;  
PID:g292938  
C;Keywords: alternative splicing; membrane protein; phosphoprotein  
F;15-94/Domain: GLGF domain homology <GLG1>

F;181-248/Domain: GLGF domain homology <GLG2>  
F;416-486/Domain: GLGF domain homology <GLG3>  
F;633-782/Domain: guanylate kinase homology <GKI>

Query Match 29.2%; Score 163.5; DB 2; Length 1736;  
Best Local Similarity 41.6%; Pred. No. 3.6e-09;  
Matches 37; Conservative 12; Mismatches 35; Indels 5; Gaps 2;  
  
Qy 7 GTFNFLGGRLMIPNTGISLLIPDAIPRGKYEIYLTLHKPEDVRLPL--AGCQTLLSPI 64  
| || | | | ||::|| | || | || : : : || :||||:  
Db 1626 GIFNSNGGVLSIETGVSIIIPQGAIPEGVEQEYFKVCRDNSILPPLDKEKGETLLSPL 1685  
  
Qy 65 VSCGPPGVLLTRPVILAMDHCGEPSDWS 93  
| ||| |: :|| | : || | :|  
Db 1686 VMCGPHGLKFLKPVELRLPHC---DPKTW 1711

RESULT 2

A46431

tight junction-associated protein ZO-1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A46431

R;Itoh, M.; Nagafuchi, A.; Yonemura, S.; Kitani-Yasuda, T.; Tsukita, S.;  
Tsukita, S.

J. Cell Biol. 121, 491-502, 1993

A;Title: The 220-kD protein colocalizing with cadherins in non-epithelial cells  
is identical to ZO-1, a tight junction-associated protein in epithelial cells:  
cDNA cloning and immunoelectron microscopy.

A;Reference number: A46431; MUID:93252986; PMID:8486731

A;Accession: A46431

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-1745 <ITO>

A;Cross-references: UNIPROT:P39447; GB:D14340; NID:g303709; PIDN:BAA03274.1;  
PID:d1003784; PID:g303710

A;Experimental source: F9 cells

A;Note: sequence extracted from NCBI backbone (NCBIN:131200, NCBIP:131201)

F;27-106/Domain: GLGF domain homology <GLG1>

F;428-498/Domain: GLGF domain homology <GLG3>

F;645-794/Domain: guanylate kinase homology <GKI>

Query Match 29.1%; Score 162.5; DB 2; Length 1745;  
Best Local Similarity 41.68%; Pred. No. 4.6e-09;  
Matches 37; Conservative 12; Mismatches 35; Indels 5; Gaps 2;  
  
Qy 7 GTFNFLGGRLMIPNTGISLLIPDAIPRGKYEIYLTLHKPEDVRLPL--AGCQTLLSPI 64  
| || | | | ||::|| | || | || : : : || :||||:  
Db 1635 GIFNSNGGVLSIETGVSIIIPQGAIPEGIEQEYFKVCRDNSILPPLDKEKGETLLSPL 1694  
  
Qy 65 VSCGPPGVLLTRPVILAMDHCGEPSDWS 93  
| ||| |: :|| | : || | :|  
Db 1695 VMCGPHGLKFLKPVELRLPHC---DPKTW 1720

RESULT 3

T32541

unc-5 protein - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32541  
R;Latreille, P.  
submitted to the EMBL Data Library, December 1997  
A;Description: The sequence of *C. elegans* cosmid B0273.  
A;Reference number: Z21187  
A;Accession: T32541  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-919 <LAT>  
A;Cross-references: UNIPROT:O44171; EMBL:AF036698; PIDN:AAB88355.1;  
GSPDB:GN00022; CESP:B0273.4a  
A;Experimental source: strain Bristol N2; clone B0273  
C;Genetics:  
A;Gene: unc-5; CESP:B0273.4a  
A;Map position: 4  
A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3  
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;  
thrombospondin type 1 repeat homology

Query Match                    17.2%; Score 96; DB 2; Length 919;  
Best Local Similarity        25.7%; Pred. No. 0.034;  
Matches    27; Conservative   21; Mismatches   47; Indels   10; Gaps    3;  
  
Qy                1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIFYEYLTLHKPEDVRLPLAGCQTL 60  
                  : | :    : | || : :| |::| |: | : :|| :    : |    ::  
Db                500 SQNIVAAQIDSNGARLSLSKGARLIVPELAVEGEKM--LYLAVIDTLDQPHLKPIESA 557  
  
Qy                61 LSPIVSCGPPGV-----LLTRPVILAMDHCGEPSP-DSWSLRL 97  
                  | ||::| |    |    :| |||::: ' ||    | |:| |    |  
Db                558 LSPVIVIGQCDVSMSAHDNILRRPVVVFRHCASTFPRDNWQFTL 602

#### RESULT 4

B44294

unc-5 protein, long form - *Caenorhabditis elegans*  
N;Contains: unc-5 protein, short form  
C;Species: *Caenorhabditis elegans*  
C;Date: 30-Apr-1993 #sequence\_revision 28-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: B44294; T32540; A44294  
R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.;  
Hedgecock, E.M.; Culotti, J.G.  
Cell 71, 289-299, 1992  
A;Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin  
type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.  
A;Reference number: A44294; MUID:93046629; PMID:1384987  
A;Contents: variety Bergerac  
A;Accession: B44294  
A;Molecule type: DNA  
A;Residues: 1-947 <LEU>  
A;Cross-references: UNIPROT:O44171; GB:S47168; NID:g258527; PIDN:AAB23867.1;  
PID:g258529  
A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670,  
NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680,  
NCBIN:116682, NCBIN:116685, NCBIP:118648)

A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation  
A;Note: mRNA lacking the first exon is equally prevalent  
R;Latreille, P.  
submitted to the EMBL Data Library, December 1997  
A;Description: The sequence of *C. elegans* cosmid B0273.  
A;Reference number: Z21187  
A;Accession: T32540  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-947 <LAT>  
A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b  
A;Experimental source: strain Bristol N2; clone B0273  
C;Genetics:  
A;Gene: unc-5  
A;Map position: 4  
A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3  
C;Function:  
A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells  
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin type 1 repeat homology  
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein  
F;30-947/Product: unc-5 protein, short form #status predicted <ALT>  
F;46-116/Domain: immunoglobulin homology <IM1>  
F;153-211/Domain: immunoglobulin homology <IM2>  
F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>  
F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>  
F;365-390/Domain: transmembrane #status predicted <TMM>  
F;512-559/Domain: SH3 homology <SH3>  
F;53-114,65-112,160-209/Disulfide bonds: #status predicted  
F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.2%; Score 96; DB 1; Length 947;  
Best Local Similarity 25.7%; Pred. No. 0.035;  
Matches 27; Conservative 21; Mismatches 47; Indels 10; Gaps 3;  
  
Qy 1 TSNMTYGTNFNLGGGLMIPNTGISLLIAPPDAIPRGKIVYEIYLTLHKPEDVRLPLAGCQL 60  
Db : | : : | || : : | |::| |: | : || : : | | ::  
Qy 528 SQNIVAAQIDSNGARLSLSKGARLIVPELAVEGEKMA--LYLAVSDTLTDQPHLKPIESA 585  
  
Qy 61 LSPIVSCGPPGV-----LLTRPVILAMDHCGEPS-DSWSLRL 97  
Db ||||: | | : | |||::: || | |::| |  
Qy 586 LSPVIVIGQCDVMSAHDNILRRPVVVVSFRHCASTFPRDNWQFTL 630

RESULT 5  
S21265  
acetylserotonin O-methyltransferase (EC 2.1.1.4) - chicken  
N;Alternate names: hydroxyindole O-methyltransferase  
C;Species: Gallus gallus (chicken)  
C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C;Accession: S21265; S22154  
R;Voisin, P.; Guerlotte, J.; Bernard, M.; Collin, J.P.; Cogne, M.  
Biochem. J. 282, 571-576, 1992

A;Title: Molecular cloning and nucleotide sequence of a cDNA encoding hydroxyindole O-methyltransferase from chicken pineal gland.  
A;Reference number: S21265; MUID:92189600; PMID:1372168  
A;Accession: S21265  
A;Molecule type: mRNA  
A;Residues: 1-346 <VOI>  
A;Cross-references: UNIPROT:Q92056; EMBL:X62309; NID:g62925; PIDN:CAA44189.1;  
PID:g62926  
C;Superfamily: O-methyltransferase  
C;Keywords: melatonin biosynthesis; methyltransferase; S-adenosylmethionine

Query Match 13.6%; Score 76; DB 2; Length 346;  
Best Local Similarity 23.8%; Pred. No. 1.6;  
Matches 30; Conservative 20; Mismatches 36; Indels 40; Gaps 6;

Qy 13 GGRL-----MIPNTGISL-----LIPP-----DAIPRGKIYE 39  
|| | : || :: |::| |:|| :|  
Db 191 GGALAQECVFLYPNCTVTIYDLPKVVQVAKERLVPPEERRIAFHEGDFFKDSIPEADLYI 250

Qy 40 IYLTLHKPEDVRLPLAGCQTLLSIV-SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRK 98  
: || :| : |: ||: :| || | :| :| :| | | :|| :|  
Db 251 LSKILHDWDDKK----CRQLLAEVYKACRPGGGVLLVESLLSEDRSGPVETQLYSLNML 305

Qy 99 KQSCEG 104  
|: ||  
Db 306 VQT-EG 310

#### RESULT 6

S37771  
ankyrin, erythrocyte - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-May-1994 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: S37771  
R;Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.  
J. Biol. Chem. 268, 9533-9540, 1993  
A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found among transcripts of the erythroid ankyrin gene.  
A;Reference number: S37771; MUID:93252825; PMID:8486643  
A;Accession: S37771  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1848 <BIR>  
A;Cross-references: UNIPROT:Q61302; EMBL:X69063; NID:g311816; PIDN:CAA48801.1;  
PID:g311817  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;48-80/Domain: ankyrin repeat homology <AN01>  
F;81-113/Domain: ankyrin repeat homology <AN02>  
F;114-146/Domain: ankyrin repeat homology <AN03>  
F;147-175/Domain: ankyrin repeat homology <AN04>  
F;176-208/Domain: ankyrin repeat homology <AN05>  
F;209-241/Domain: ankyrin repeat homology <AN06>  
F;242-274/Domain: ankyrin repeat homology <AN07>  
F;275-307/Domain: ankyrin repeat homology <AN08>  
F;308-340/Domain: ankyrin repeat homology <AN09>

F;341-373/Domain: ankyrin repeat homology <AN10>  
 F;374-406/Domain: ankyrin repeat homology <AN11>  
 F;407-439/Domain: ankyrin repeat homology <AN12>  
 F;440-472/Domain: ankyrin repeat homology <AN13>  
 F;473-505/Domain: ankyrin repeat homology <AN14>  
 F;506-538/Domain: ankyrin repeat homology <AN15>  
 F;539-571/Domain: ankyrin repeat homology <AN16>  
 F;572-604/Domain: ankyrin repeat homology <AN17>  
 F;605-637/Domain: ankyrin repeat homology <AN18>  
 F;638-670/Domain: ankyrin repeat homology <AN19>  
 F;671-703/Domain: ankyrin repeat homology <AN20>  
 F;704-736/Domain: ankyrin repeat homology <AN21>  
 F;737-769/Domain: ankyrin repeat homology <AN22>  
 F;770-802/Domain: ankyrin repeat homology <AN23>

Query Match                    13.1%; Score 73; DB 2; Length 1848;  
 Best Local Similarity    33.3%; Pred. No. 22;  
 Matches    23; Conservative    11; Mismatches    27; Indels    8; Gaps    3;

Qy	20 NTGISLLIPPD--AIPRGK <del>I</del> Y <del>E</del> IYLTLHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT	75
	:   : ::              : :     :      ::	
Db	943 HNGLRVVIPPRTCAAPT----RITCRLVKPQKLNTPPPLAEEGLASRIIALGPTGAQFL	998

Qy	76 RPVILAMDH	84
	: :	
Db	999 SPVIVEIPH	1007

RESULT 7  
I49502  
ankyrin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I49502  
R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.  
Mamm. Genome 3, 281-285, 1992  
A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain.  
A;Reference number: I49502; MUID:92345717; PMID:1386265  
A;Accession: I49502  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1862 <RES>  
A;Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1;  
PID:g191940  
C;Genetics:  
A;Gene: Ank-1  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;40-72/Domain: ankyrin repeat homology <AN01>  
F;73-105/Domain: ankyrin repeat homology <AN02>  
F;106-138/Domain: ankyrin repeat homology <AN03>  
F;139-167/Domain: ankyrin repeat homology <AN04>  
F;168-200/Domain: ankyrin repeat homology <AN05>  
F;201-233/Domain: ankyrin repeat homology <AN06>  
F;234-266/Domain: ankyrin repeat homology <AN07>  
F;267-299/Domain: ankyrin repeat homology <AN08>

F;300-332/Domain: ankyrin repeat homology <AN09>  
F;333-365/Domain: ankyrin repeat homology <AN10>  
F;366-398/Domain: ankyrin repeat homology <AN11>  
F;399-431/Domain: ankyrin repeat homology <AN12>  
F;432-464/Domain: ankyrin repeat homology <AN13>  
F;465-497/Domain: ankyrin repeat homology <AN14>  
F;498-530/Domain: ankyrin repeat homology <AN15>  
F;531-563/Domain: ankyrin repeat homology <AN16>  
F;564-596/Domain: ankyrin repeat homology <AN17>  
F;597-629/Domain: ankyrin repeat homology <AN18>  
F;630-662/Domain: ankyrin repeat homology <AN19>  
F;663-695/Domain: ankyrin repeat homology <AN20>  
F;696-728/Domain: ankyrin repeat homology <AN21>  
F;729-761/Domain: ankyrin repeat homology <AN22>  
F;762-794/Domain: ankyrin repeat homology <AN23>

Query Match 13.1%; Score 73; DB 2; Length 1862;  
Best Local Similarity 33.3%; Pred. No. 23;  
Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIFYEYLTLHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75  
: |: ::||| || | | | ||: : ||| : | | |:: |||  
Db 927 HNGLRVVIPPRTCAAPT----RITCRLVKPQLNTPPLAEEEGLASRIIALGPTGAQFL 982  
  
Qy 76 RPVILAMDH 84  
|||: : |  
Db 983 SPVIVEIPH 991

RESULT 8  
B35049

ankyrin 1, erythrocyte splice form 3 - human  
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N;Contains: ankyrin 2.2, erythrocyte  
C;Species: Homo sapiens (man)  
C;Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998  
C;Accession: B35049  
R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A;Title: cDNA sequence for human erythrocyte ankyrin.  
A;Reference number: A35049; MUID:90175370; PMID:1689849  
A;Accession: B35049  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1856 <LAM>  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:118737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>  
F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F;44-76/Domain: ankyrin repeat homology <AN01>  
F;77-109/Domain: ankyrin repeat homology <AN02>  
F;110-142/Domain: ankyrin repeat homology <AN03>

F;143-171/Domain: ankyrin repeat homology <AN04>  
F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 12.9%; Score 72; DB 2; Length 1856;  
Best Local Similarity 33.3%; Pred. No. 29;  
Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIIYEIYLTLHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75  
: |: ::||| || | | | ||: : ||| : | | |:: |||  
Db 931 HNGLRVVIPPRTCAAPT---RITCRLVKPQLSTPPPLAEELASRIIALGPTGAQFL 986

Qy 76 RPVILAMDH 84  
|||: : |  
Db 987 SPVIVEIIPH 995

RESULT 9

A35049  
ankyrin 1, erythrocyte splice form 2 - human  
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N;Contains: ankyrin 2.2, erythrocyte  
C;Species: Homo sapiens (man)  
C;Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 09-Jul-2004  
C;Accession: A35049  
R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Kan, Y.W.; Palek, J.  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A;Title: cDNA sequence for human erythrocyte ankyrin.  
A;Reference number: A35049; MUID:90175370; PMID:1689849  
A;Accession: A35049  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1880 <LAM>  
A;Cross-references: UNIPROT:P16157; GB:M28880  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:118737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing; cytoskeleton  
F;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>  
F;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F;44-76/Domain: ankyrin repeat homology <AN01>  
F;77-109/Domain: ankyrin repeat homology <AN02>  
F;110-142/Domain: ankyrin repeat homology <AN03>  
F;143-171/Domain: ankyrin repeat homology <AN04>  
F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 12.9%; Score 72; DB 2; Length 1880;  
Best Local Similarity 33.3%; Pred. No. 29;  
Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;

Qy 20 NTGISLLIPPD--AIPRGKIYIYLTLHKPEDVRL--PLAGCQTLLSPLVSCGPPGVLLT 75  
: |: ::||| || | | | ||: : ||| : | | |:: |||  
Db 931 HNGLRVVIPPRTCAAPT---RITCRLVKPQLSTPPPLAEELASRIIALGPTGAQFL 986  
,

Qy 76 RPVILAMDH 84  
|||: : |  
Db 987 SPVIVEIPH 995

## RESULT 10

SJHUK

ankyrin 1, erythrocyte splice form 1 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C;Accession: S08275; A33219; PC2220; A35443

R;Lux, S.E.; John, K.M.; Bennett, V.

Nature 344, 36-42, 1990

A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.

A;Reference number: S08275; MUID:90158830; PMID:2137557

A;Accession: S08275

A;Molecule type: mRNA

A;Residues: 1-1881 <LUL>

A;Cross-references: UNIPROT:P16157; EMBL:X16609; NID:g28701; PIDN:CAA34610.1;  
PID:g28702  
A;Accession: A33219  
A;Molecule type: protein  
A;Residues: 2-7,'X',9-17,'X',19-20,'T',22-30;733-749,'A',751-753;828-  
833,'X',835-855,'X',857-859,'XX',862-871;959-1003;1106-1120,'XX',1123-1128;1149-  
1172;1282-1285,'E',1287-1288;1307-1332;1345-1365,'X',1367;1383-1427;1601-  
1630;1686-1698,'D',1700;1763-1772 <LUX>  
A;Note: 845-Arg and 1392-Thr were also found  
R;Hermann, J.; Barel, M.; Frade, R.  
Biochem. Biophys. Res. Commun. 204, 453-460, 1994  
A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57  
membrane proteinase which cleaves C3, the third component of complement.  
A;Reference number: PC2220; MUID:95071348; PMID:7526850  
A;Accession: PC2220  
A;Molecule type: protein  
A;Residues: 910-929 <HER>  
R;Davis, L.H.; Bennett, V.  
J. Biol. Chem. 265, 10589-10596, 1990  
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion  
exchanger and spectrin.  
A;Reference number: A35443; MUID:90285190; PMID:2141335  
A;Accession: A35443  
A;Molecule type: protein  
A;Residues: 'X',5,'X',7-12;403-417,'X',419-422,'H',424,'LQ';797-800,'L',802-  
814;862-863,'X',865-877;'X',899-901,'T',903-909,'X',911-912 <DAV>  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:118737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing; phosphoprotein  
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>  
F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>  
F;2-827/Domain: 89K #status predicted <DOM1>  
F;2-827/Region: anion exchange protein binding  
F;44-76/Domain: ankyrin repeat homology <AN01>  
F;77-109/Domain: ankyrin repeat homology <AN02>  
F;110-142/Domain: ankyrin repeat homology <AN03>  
F;143-171/Domain: ankyrin repeat homology <AN04>  
F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>

F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>  
F;828-1382/Domain: 62K #status predicted <DOM2>  
F;828-1382/Region: spectrin binding  
F;1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 12.9%; Score 72; DB 1; Length 1881;  
Best Local Similarity 33.3%; Pred. No. 29;  
Matches 23; Conservative 11; Mismatches 27; Indels 8; Gaps 3;  
  
Qy 20 NTGISLLIPPD--AIPRGKIYEIYLTLHKPEDVRL--PLAGCQTLLSPIVSCGPPGVLLT 75  
: |: ::||| || | | | | ||: : ||| : || | |:: |||  
Db 931 HNGLRVVIPPRTCAAPT---RITCRLVKPQLSTPPPLAEEGLASRIIALGPTGAQFL 986  
  
Qy 76 RPVILAMDH 84  
|||: : |  
Db 987 SPVIVEIPH 995

RESULT 11  
S73122  
carbamoyl phosphate synthase small chain - red alga (*Porphyra purpurea*)  
chloroplast  
C;Species: chloroplast *Porphyra purpurea*  
C;Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
C;Accession: S73122  
R;Reith, M.; Munholland, J.  
Plant Mol. Biol. Rep. 13, 333-335, 1995  
A;Title: Complete nucleotide sequence of the *Porphyra purpurea* chloroplast genome.  
A;Reference number: S73108  
A;Accession: S73122  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-384 <REI>  
A;Cross-references: UNIPROT:P51201; EMBL:U38804; NID:g1276652; PIDN: AAC08087.1; PID:g1276667  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
C;Genetics:  
A;Gene: carA  
A;Genome: chloroplast  
C;Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology  
C;Keywords: chloroplast  
F;9-373/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology <CPS>  
F;197-373/Domain: trpG homology <TRG>  
F;272/Active site: Cys #status predicted

Query Match 12.5%; Score 70; DB 2; Length 384;  
Best Local Similarity 24.3%; Pred. No. 8.1;  
Matches 27; Conservative 20; Mismatches 26; Indels 38; Gaps 6;  
  
Qy 17 MIPNTGISLLIPPD--AIP-----RGKIYE-----IYLTLHKPEDVRLPLAG 56  
:|||| ::: | ::| | ||| : | : : |||

Db 161 LIPNVTTNIMYDWDEKSLPSWYLADRNREKIYSQLKVIVIDFGVKLNILR---RLATLG 216  
Qy 57 CQTLSP-----IVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQ 100  
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Db 217 CQITVMPASTPTQDILSCKPDGILLS-----NGPGDPSAVNYGIKTVKE 260

RESULT 12

D72240

tRNA guanine transglycosylase - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: D72240

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: D72240

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-369 <ARN>

A;Cross-references: UNIPROT:Q9X1P7; GB:AE001801; GB:AE000512; NID:g4982114; PIDN:AAD36627.1; PID:g4982128; TIGR:TM1561

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1561

C;Superfamily: queuine tRNA-ribosyltransferase

Query Match 12.4%; Score 69.5; DB 2; Length 369;  
Best Local Similarity 23.9%; Pred. No. 8.8;  
Matches 26; Conservative 19; Mismatches 35; Indels 29; Gaps 6;

Qy 7 GTFNFLGGR--LMIPNTGISLLIPPDIAIPRGKIYEIYLTLHKPEDV--RLPLAGCQTLLS 62  
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Db 75 GLHNFMGWKRPILTDGGFQVF---SLPKIRIDD-----EGVVFRSPIDGSKVFLN 122

Qy 63 PIVSCGPPGVLLTRPVILAMDHCGEPSD-----SWSLRLKK 99

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Db 123 PEISM-EVQIALGSDICMVFDHCPVPDADYEEVKEATERTYRWALRSKK 170

RESULT 13

I48780

Stral/Eplg2 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: I48780; A55507; A55062; S52670

R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Dolle, P.; Chambon, P.

Dev. Biol. 170, 420-433, 1995

A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells and characterization of a novel mouse gene, Stral (mouse LERK-2/Eplg2).  
A;Reference number: I48780; MUID:95377533; PMID:7649373  
A;Accession: I48780  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-345 <RES>  
A;Cross-references: UNIPROT:P52795; EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859  
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Davison, B.L. Genomics 24, 127-132, 1994  
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a binding protein for the receptor tyrosine kinase Elk.  
A;Reference number: A55507; MUID:95203867; PMID:7896266  
A;Accession: A55507  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-345 <FLE>  
A;Cross-references: GB:U07598  
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M. J. Biol. Chem. 269, 26606-26609, 1994  
A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase.  
A;Reference number: A55062; MUID:95014510; PMID:7929389  
A;Accession: A55062  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-89, 'T', 91-345 <SHA>  
A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929  
C;Genetics:  
A;Gene: EPLG2

Query Match 12.3%; Score 69; DB 2; Length 345;  
Best Local Similarity 30.9%; Pred. No. 9.3;  
Matches 29; Conservative 11; Mismatches 40; Indels 14; Gaps 5;  
  
Qy 11 FLGGR--LMIPNTGISLLIIPPDAIPRGKIYEIY-LTLHKPEDVRLPLAGCQTLSP--IV 65  
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Db 44 FLSGKGLVIYPKIGDKLDIICPRAEAGR PYEYYKLYLVRPEQA---AACSTVLDPNVLV 99  
  
Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKK 99  
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Db 100 TCNKPHQEIRFTIKFQ----EFSPNYMGLEFKK 128

RESULT 14  
I58406  
LERK-2 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I58406  
R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollingsworth, T.; VandenBos, T.; Davison, B.L.; Lyman, S.D.; Beckmann, M.P. Oncogene 9, 3241-3248, 1994

A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved and expressed in a developmentally regulated pattern.  
A;Reference number: I58406; MUID:95022634; PMID:7936648  
A;Accession: I58406  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-345 <RES>  
A;Cross-references: UNIPROT:P52796; EMBL:U07560; NID:g563118; PIDN:AAA53092.1;  
PID:g563119  
C;Genetics:  
A;Gene: Eplg2

Query Match 12.3%; Score 69; DB 2; Length 345;  
Best Local Similarity 31.9%; Pred. No. 9.3;  
Matches 30; Conservative 10; Mismatches 40; Indels 14; Gaps 5;  
  
Qy 11 FLGGR--LMIPNTGISLLIIPPDAIPRGKIYEIY-LTLHKPEDVRLPLAGCQTLLSP--IV 65  
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Db 44 FLSGKGLVIYPKIGDKLDIICPRAEAGR PYEYYKLYLVRPEQA---AACSTVLDPNVLV 99  
  
Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKK 99  
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Db 100 TCNKP----QQEIRFTIKFQEFS PNYMGLEFKK 128

RESULT 15  
S46993  
elk ligand - human  
C;Species: Homo sapiens (man)  
C;Date: 15-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S46993  
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlosky, C.; Hollingsworth, T.; Shilling, H.; Maraskovsky, E.; Fletcher, F.A.; Lhotak, V.; Pawson, T.; Lyman, S.D.  
EMBO J. 13, 3757-3762, 1994  
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kinase receptors.  
A;Reference number: S46993; MUID:94349923; PMID:8070404  
A;Accession: S46993  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-346 <BEC>  
A;Cross-references: UNIPROT:P98172; GB:U09304; NID:g538366; PIDN:AAA53093.1;  
PID:g538367

Query Match 12.2%; Score 68; DB 2; Length 346;  
Best Local Similarity 30.9%; Pred. No. 12;  
Matches 29; Conservative 11; Mismatches 40; Indels 14; Gaps 5;  
  
Qy 11 FLGGR--LMIPNTGISLLIIPPDAIPRGKIYEIY-LTLHKPEDVRLPLAGCQTLLSP--IV 65  
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Db 44 FLSGKGLVIYPKIGDKLDIICPRAEAGR PYEYYKLYLVRPEQA---AACSTVLDPNVLV 99  
  
Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKK 99  
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Db 100 TCNRPEQEIRFTIKFQ----EFSP NYMGLEFKK 128

Search completed: March 1, 2005, 09:07:22  
Job time : 5.05992 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 20.0163 Seconds  
(without alignments)  
1704.439 Million cell updates/sec

Title: US-10-624-932-2\_COPY\_495\_598  
Perfect score: 559  
Sequence: 1 TSNMTYGTFNFLGGRLMIPN.....CGEPSPDSWSLRKKQSCEG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

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20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	559	100.0	544	10	US-09-970-944-14	Sequence 14, Appl
2	559	100.0	842	15	US-10-311-623-1	Sequence 1, Appl
3	559	100.0	898	10	US-09-918-779-2	Sequence 2, Appl
4	559	100.0	898	15	US-10-624-932-2	Sequence 2, Appl
5	559	100.0	899	10	US-09-970-944-2	Sequence 2, Appl
6	555	99.3	436	15	US-10-296-115-1104	Sequence 1104, Ap
7	553	98.9	557	10	US-09-933-261-6	Sequence 6, Appl
8	553	98.9	557	14	US-10-256-702-6	Sequence 6, Appl
9	553	98.9	898	10	US-09-933-261-5	Sequence 5, Appl
10	553	98.9	898	10	US-09-970-944-13	Sequence 13, Appl
11	553	98.9	898	14	US-10-256-702-5	Sequence 5, Appl
12	553	98.9	898	14	US-10-240-154-16	Sequence 16, Appl
13	348	62.3	931	10	US-09-970-944-15	Sequence 15, Appl
14	348	62.3	931	11	US-09-972-211-121	Sequence 121, App
15	348	62.3	931	15	US-10-087-684-35	Sequence 35, Appl
16	348	62.3	931	15	US-10-037-417-117	Sequence 117, App
17	348	62.3	931	15	US-10-096-625-121	Sequence 121, App
18	348	62.3	1010	15	US-10-218-779-35	Sequence 35, Appl
19	337	60.3	931	10	US-09-970-944-16	Sequence 16, Appl
20	337	60.3	931	10	US-09-970-944-17	Sequence 17, Appl
21	337	60.3	931	11	US-09-972-211-122	Sequence 122, App
22	337	60.3	931	11	US-09-972-211-125	Sequence 125, App
23	337	60.3	931	15	US-10-087-684-36	Sequence 36, Appl
24	337	60.3	931	15	US-10-218-779-36	Sequence 36, Appl
25	337	60.3	931	15	US-10-037-417-118	Sequence 118, App
26	337	60.3	931	15	US-10-037-417-119	Sequence 119, App
27	337	60.3	931	15	US-10-037-417-120	Sequence 120, App
28	337	60.3	931	15	US-10-096-625-122	Sequence 122, App
29	337	60.3	931	15	US-10-096-625-125	Sequence 125, App
30	287	51.3	223	9	US-09-764-870-436	Sequence 436, App
31	287	51.3	223	14	US-10-125-540-436	Sequence 436, App
32	287	51.3	554	15	US-10-108-260A-2682	Sequence 2682, Ap
33	287	51.3	933	15	US-10-087-684-2	Sequence 2, Appl
34	287	51.3	933	15	US-10-087-684-4	Sequence 4, Appl
35	287	51.3	933	15	US-10-218-779-2	Sequence 2, Appl
36	287	51.3	933	15	US-10-218-779-4	Sequence 4, Appl
37	287	51.3	945	14	US-10-028-072-146	Sequence 146, App
38	287	51.3	945	14	US-10-140-808-146	Sequence 146, App
39	287	51.3	945	14	US-10-121-049-146	Sequence 146, App
40	287	51.3	945	14	US-10-123-904-146	Sequence 146, App
41	287	51.3	945	14	US-10-140-470-146	Sequence 146, App
42	287	51.3	945	14	US-10-175-746-146	Sequence 146, App
43	287	51.3	945	14	US-10-176-918-146	Sequence 146, App
44	287	51.3	945	14	US-10-176-921-146	Sequence 146, App
45	287	51.3	945	14	US-10-137-865-146	Sequence 146, App

#### ALIGNMENTS

RESULT 1  
 US-09-970-944-14  
 ; Sequence 14, Application US/09970944  
 ; Publication No. US20030204052A1

; GENERAL INFORMATION:  
; APPLICANT: Herrman, John L  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Shimkets, Richard A  
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and  
; TITLE OF INVENTION: Antibodies Directed Against these Proteins  
; FILE REFERENCE: 21402-138  
; CURRENT APPLICATION NUMBER: US/09/970,944  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/237,862  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 544  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-970-944-14

Query Match 100.0%; Score 559; DB 10; Length 544;  
Best Local Similarity 100.0%; Pred. No. 2.6e-56;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
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Db 201 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 244

RESULT 2

US-10-311-623-1

; Sequence 1, Application US/10311623

; Publication No. US20040023244A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.  
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.  
; APPLICANT: YUE, Henry; NGUYEN, Danniel B.  
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.  
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda  
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.  
; APPLICANT: YAO, Monique G.; BURFORD, Neil  
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.  
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.  
; APPLICANT: YANG, Junming; XU, Yuming  
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.  
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.  
; APPLICANT: DUGGAN, Brendan M.; LU, Yan  
; TITLE OF INVENTION: RECEPTORS  
; FILE REFERENCE: PF-0793 USN  
; CURRENT APPLICATION NUMBER: US/10/311,623  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US 01/19942  
; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: US 60/214,027  
; PRIOR FILING DATE: 2000-06-21  
; PRIOR APPLICATION NUMBER: US 60/228,045  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/255,104  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 842  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CD1  
US-10-311-623-1

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Best Local Similarity 100.0%; Pred. No. 4.5e-56;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 439 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 498

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
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Db 499 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 542

### RESULT 3

US-09-918-779-2

; Sequence 2, Application US/09918779  
; Publication No. US20030064369A1  
; GENERAL INFORMATION:  
; APPLICANT: Taupier, Raymond  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Spaderna, Steven  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Grosse, William  
; APPLICANT: Alsobrook, John  
; APPLICANT: Lepley, Denise  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John  
; APPLICANT: Stone, David  
; APPLICANT: Smithson, Glennda  
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-074 US  
; CURRENT APPLICATION NUMBER: US/09/918,779

; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/221,409  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/222,840  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,752  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/223,762  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/223,770  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/223,769  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/225,146  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,392  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: 60/225,470  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: 60/225,697  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/263,662  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/281,645  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 898  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-918-779-2

Query Match 100.0%; Score 559; DB 10; Length 898;  
Best Local Similarity 100.0%; Pred. No. 4.9e-56;  
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Db 495 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
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Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 598

#### RESULT 4

US-10-624-932-2

; Sequence 2, Application US/10624932  
; Publication No. US20040096877A1  
; GENERAL INFORMATION:  
; APPLICANT: Taupier, Raymond  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Spaderna, Steven  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Zerhusen, Bryan

; APPLICANT: Spytek, Kimberly  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Grosse, William  
; APPLICANT: Alsobrook, John  
; APPLICANT: Lepley, Denise  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John  
; APPLICANT: Stone, David  
; APPLICANT: Smithson, Glennda  
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-074 US  
; CURRENT APPLICATION NUMBER: US/10/624,932  
; CURRENT FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: 09/918,779  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 60/221,409  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/222,840  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,752  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/223,762  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/223,770  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/223,769  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/225,146  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,392  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: 60/225,470  
; PRIOR FILING DATE: 2000-08-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 898  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-624-932-2

Query Match 100.0%; Score 559; DB 15; Length 898;  
Best Local Similarity 100.0%; Pred. No. 4.9e-56;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| |||||||  
Db 495 TSNMTYGTNFNLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
| |||||||  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| |||||||  
Db 555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598



; ORGANISM: Homo sapiens  
US-10-296-115-1104

Query Match 99.3%; Score 555; DB 15; Length 436;  
Best Local Similarity 99.0%; Pred. No. 5.9e-56;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 32 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 91  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 92 LSPIVSCGPPGVLLTRPVILGMDHCGEPSDWSLRLKKQSCEG 135

RESULT 7

US-09-933-261-6

; Sequence 6, Application US/09933261  
; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc  
; Leonardo, E. David  
; Hink, Lindsay  
; Masu, Masayuki  
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261  
; FILING DATE: 20-Aug-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/808,982  
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 557 amino acids

; TYPE: amino acid  
; STRANDEDNESS: No. US20030040046A1 Relevant  
; TOPOLOGY: No. US20030040046A1 Relevant  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-933-261-6

Query Match 98.9%; Score 553; DB 10; Length 557;  
Best Local Similarity 99.0%; Pred. No. 1.4e-55;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNFGGLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 153 TSNMTYGTNFNFGGLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 212

Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 213 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLALKQSCEG 256

RESULT 8  
US-10-256-702-6  
; Sequence 6, Application US/10256702  
; Publication No. US20030059859A1  
; GENERAL INFORMATION:  
; APPLICANT: Tessier-Lavigne, Marc  
; Leonardo, E. David  
; Hink, Lindsay  
; Masu, Masayuki  
; Kazuko, Keino-Masu  
; TITLE OF INVENTION: Netrin Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/256,702  
; FILING DATE: 27-Sep-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/933,261  
; FILING DATE: 20-Aug-2001  
; APPLICATION NUMBER: 08/808,982  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:  
;     TELEPHONE: (415) 343-4341  
;     TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 6:  
;     SEQUENCE CHARACTERISTICS:  
;     LENGTH: 557 amino acids  
;     TYPE: amino acid  
;     STRANDEDNESS: No. US20030059859A1 Relevant  
;     TOPOLOGY: No. US20030059859A1 Relevant  
;     MOLECULE TYPE: peptide  
;     SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-256-702-6

Query Match               98.9%; Score 553; DB 14; Length 557;  
Best Local Similarity   99.0%; Pred. No. 1.4e-55;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy           1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQL 60  
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db           153 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQL 212  
  
Qy           61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
            ||||||||||||||||||||||||||||||||||| |||||||||  
Db           213 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLALKQSCEG 256

RESULT 9  
US-09-933-261-5  
; Sequence 5, Application US/09933261  
; Publication No. US20030040046A1  
; GENERAL INFORMATION:  
;     APPLICANT: Tessier-Lavigne, Marc  
;           Leonardo, E. David  
;           Hink, Lindsay  
;           Masu, Masayuki  
;           Kazuko, Keino-Masu  
; TITLE OF INVENTION: Netrin Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
;     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
;     STREET: 268 BUSH STREET, SUITE 3200  
;     CITY: SAN FRANCISCO  
;     STATE: CALIFORNIA  
;     COUNTRY: USA  
;     ZIP: 94104  
; COMPUTER READABLE FORM:  
;     MEDIUM TYPE: Floppy disk  
;     COMPUTER: IBM PC compatible  
;     OPERATING SYSTEM: PC-DOS/MS-DOS  
;     SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
;     APPLICATION NUMBER: US/09/933,261  
;     FILING DATE: 20-Aug-2001  
;     CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
;     APPLICATION NUMBER: 08/808,982  
;     FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 898 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. US20030040046A1 Relevant  
TOPOLOGY: No. US20030040046A1 Relevant

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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Query Match          98.9%; Score 553; DB 10; Length 898;
Best Local Similarity 98.1%; Pred. No. 2.5e-55;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60
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Db      495 TSNMAYGTNFNLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 554

Qy      61 LSPIVSCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 104
        ||||:|||||||||||||||||||||||||||||||||||||
Db      555 LSPVVSCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 598

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RESULT 10  
US-09-970-944-13  
; Sequence 13, Application US/09970944  
; Publication No. US20030204052A1  
; GENERAL INFORMATION:  
; APPLICANT: Herrman, John L  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Shimkets, Richard A  
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and  
; TITLE OF INVENTION: Antibodies Directed Against these Proteins  
; FILE REFERENCE: 21402-138  
; CURRENT APPLICATION NUMBER: US/09/970,944  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/237,862  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 898  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-970-944-13

Query Match 98.9%; Score 553; DB 10; Length 898;  
Best Local Similarity 98.1%; Pred. No. 2.5e-55;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 495 TSNMAYGTNFNLGGRLMIPNTGISLLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 555 LSPVVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 11

US-10-256-702-5

; Sequence 5, Application US/10256702

; Publication No. US20030059859A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc  
; Leonardo, E. David  
; Hink, Lindsay  
; Masu, Masayuki  
; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/256,702  
; FILING DATE: 27-Sep-2002  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/933,261  
; FILING DATE: 20-Aug-2001  
; APPLICATION NUMBER: 08/808,982  
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 898 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. US20030059859A1 Relevant  
; TOPOLOGY: No. US20030059859A1 Relevant  
; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-256-702-5

Query Match 98.9%; Score 553; DB 14; Length 898;  
Best Local Similarity 98.1%; Pred. No. 2.5e-55;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
Db 495 TSNMAYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
Db 555 LSPVVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 12

US-10-240-154-16

; Sequence 16, Application US/10240154

; Publication No. US20030175741A1

; GENERAL INFORMATION:

; APPLICANT: Cochran et al.

; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES

; FILE REFERENCE: CKFW-P01-006

; CURRENT APPLICATION NUMBER: US/10/240,154

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: PCT/GB01/01486

; PRIOR FILING DATE: 2001-04-02

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 898

; TYPE: PRT

; ORGANISM: Rattus sp.

US-10-240-154-16

Query Match 98.9%; Score 553; DB 14; Length 898;  
Best Local Similarity 98.1%; Pred. No. 2.5e-55;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 60  
Db 495 TSNMAYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTL 554  
  
Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
Db 555 LSPVVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598

RESULT 13

US-09-970-944-15

; Sequence 15, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding  
Same and  
; TITLE OF INVENTION: Antibodies Directed Against these Proteins  
; FILE REFERENCE: 21402-138  
; CURRENT APPLICATION NUMBER: US/09/970,944  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 60/237,862  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 931  
; TYPE: PRT  
; ORGANISM: *Caenorhabditis elegans*  
US-09-970-944-15

Query Match 62.3%; Score 348; DB 10; Length 931;  
Best Local Similarity 58.6%; Pred. No. 2.1e-31;  
Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIPPDAlPRGKIYEIYLTLHKPEDVRLPLAGCQTLLSPIV 65  
:||||| ||| |:|||:|:||| | |||:|:|||:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 533 FGTFNSLGGHIIIPNSGVSLIPAGAI PQGRVYEMYVTVHRKENMRPPMEDSQTLTPVV 592  
  
Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 104  
||||||| ||||||| : || :|| : | :|| |: :|  
Db 593 SCGPPGALLTRPVILTLHHCADPSTEDWKIQLKNQAVQG 631

#### RESULT 14

US-09-972-211-121

; Sequence 121, Application US/09972211  
; Publication No. US20040048245A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard A  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Zerhusen, Bryan D  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Malyankar, Uriel M  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Spytek, Kimberly Ann  
; APPLICANT: Li, Li  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Ellerman, Karen  
; APPLICANT: MacDougall, John R  
; APPLICANT: Gunther, Erik  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David J  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Szekeres Jr, Edward S  
; TITLE OF INVENTION: No. US20040048245A1 Human Proteins, Polynucleotides  
Encoding Them And

; TITLE OF INVENTION: Methods Of Using The Same  
; FILE REFERENCE: 21402-141  
; CURRENT APPLICATION NUMBER: US/09/972,211  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 60/238,325  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,323  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,400  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,397  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,401  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,379  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,402  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 30/238,384  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,373  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,372  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,383  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,382  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/275,892  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/296,860  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 198  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 121  
; LENGTH: 931  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-972-211-121

Query Match 62.3%; Score 348; DB 11; Length 931;  
Best Local Similarity 58.6%; Pred. No. 2.1e-31;  
Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;  
  
Qy 6 YGTFNFLGGRLMIPNTGISLLIIPPDAIPRGKIEIYLTLLHKPEDVRLPLAGCQTLLSPIV 65  
Db :||||| ||| |:|||:|:||||| |||:|:|||:|:|:|:|:|:|:|:|:|:  
Qy 533 FGTFNLSLGGHLIIPNSGVSLIIPAGAIPQGRVYEMYVTVHRKENMRPPMEDSQTLTTPVV 592  
Db ||||||| ||||||| : || :|| : | :|| |: :|  
Qy 66 SCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
Db ||||||| ||||||| : || :|| : | :|| |: :|  
Qy 593 SCGPPGALLTRPVILTLHHCADPSTEDWKIQLKNQAVQG 631

RESULT 15  
US-10-087-684-35  
; Sequence 35, Application US/10087684  
; Publication No. US20040029116A1

; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Cathereine E.  
; APPLICANT: Casman, Stacie, J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Guo, Xiaojaia  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gangolli, Esha A.  
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-214 CIP  
; CURRENT APPLICATION NUMBER: US/10/087,684  
; CURRENT FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 35  
; LENGTH: 931  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-087-684-35  
  
Query Match 62.3%; Score 348; DB 15; Length 931;  
Best Local Similarity 58.6%; Pred. No. 2.1e-31;  
Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;  
  
Qy 6 YGTFNFLGGRLMIPNTGISLLIIPPDAIPRGKIFYEIYLTLLHKPEDVRLPLAGCQTLLSPIV 65  
:||||| ||| |:|||:|:||||| |||:||:|||:||:|: ||:| |: ||||:||:  
Db 533 FGTFNSLGGHIIIPNSGVSLIIPAGAI PQGRVYEMYVTVHRKENMRPPMEDSQTLT PVV 592

Qy        66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 104  
          ||||||| |||||||| : || :|| : | ::|| |: :|  
Db        593 SCGPPGALLTRPVILTLHHCADPSTEDWKIQLKNQAVQG 631

Search completed: March 1, 2005, 09:51:32  
Job time : 21.0163 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 19.025 Seconds  
(without alignments)  
2799.282 Million cell updates/sec

Title: US-10-624-932-2\_COPY\_495\_598  
Perfect score: 559  
Sequence: 1 TSNMTYGTFNFLGGRLMIPN.....CGEPSPDSWSLRLKKQSCEG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	559	100.0	842	1	UN5A_HUMAN Q6zn44 homo sapien
2	554	99.1	898	1	UN5A_MOUSE Q8kls4 mus musculu
3	553	98.9	898	1	UN5A_RAT O08721 rattus norv
4	348	62.3	931	1	UN5C_MOUSE O08747 mus musculu
5	346	61.9	931	1	UN5C_CHICK Q7t2z5 gallus gall
6	345	61.7	931	1	UN5C_RAT Q761x5 rattus norv
7	337	60.3	931	1	UN5C_HUMAN O95185 homo sapien
8	309	55.3	943	1	UN5B_XENLA Q8jgt4 xenopus lae
9	287	51.3	945	1	UN5B_HUMAN Q8izj1 homo sapien
10	277	49.6	945	1	UN5B_RAT O08722 rattus norv
11	274	49.0	945	1	UN5B_MOUSE Q8kls3 mus musculu
12	245.5	43.9	956	1	UN5D_MOUSE Q8kls2 mus musculu
13	243.5	43.6	953	1	UN5D_HUMAN Q6uxz4 homo sapien
14	192	34.3	1267	2	Q68DX9 Q68dx9 homo sapien
15	192	34.3	1769	2	O97758 canis famil

16	191	34.2	757	2	Q91YW2	Q91yw2 mus musculu
17	184	32.9	1692	2	Q6MZU1	Q6mzu1 homo sapien
18	163.5	29.2	1736	1	ZO1_HUMAN	Q07157 homo sapien
19	162.5	29.1	1745	1	ZO1_MOUSE	P39447 mus musculu
20	155.5	27.8	2134	2	Q7QAT6	Q7qat6 anopheles g
21	145.5	26.0	518	2	Q8IV45	Q8iv45 homo sapien
22	142.5	25.5	1695	2	Q9BKL2	Q9bkl2 hydra atten
23	139.5	25.0	2090	2	Q9VHK3	Q9vhk3 drosophila
24	135.5	24.2	518	2	Q6R653	Q6r653 mus musculu
25	133.5	23.9	876	2	Q7PW78	Q7pw78 anopheles g
26	116	20.8	149	2	Q7YS63	Q7ys63 sus scrofa
27	101.5	18.2	759	2	Q7PW77	Q7pw77 anopheles g
28	98.5	17.6	1109	2	Q8I103	Q8i103 caenorhabdi
29	96	17.2	919	1	UNC5_CAEEL	Q26261 caenorhabdi
30	86	15.4	1072	1	UNC5_DROME	Q95tu8 drosophila
31	80.5	14.4	370	2	Q72J31	Q72j31 thermus the
32	78	14.0	110	2	Q8QN46	Q8qn46 cowpox viru
33	76.5	13.7	715	2	Q8IZW8	Q8izw8 homo sapien
34	76	13.6	230	2	Q6ZQQ7	Q6zqq7 homo sapien
35	76	13.6	258	2	Q7WZ45	Q7wz45 nonomuraea
36	76	13.6	346	1	HIOM_CHICK	Q92056 gallus gall
37	74.5	13.3	374	2	Q6H6C9	Q6h6c9 oryza sativ
38	74	13.2	121	2	Q8JTG1	Q8jtg1 cowpox viru
39	74	13.2	133	2	Q6ZBE3	Q6zbe3 oryza sativ
40	73.5	13.1	1330	2	Q7R3T6	Q7r3t6 giardia lam
41	73	13.1	1098	2	Q61304	Q61304 mus musculu
42	73	13.1	1136	2	Q9N180	Q9n180 bos taurus
43	73	13.1	1848	2	Q61302	Q61302 mus musculu
44	73	13.1	1862	1	ANK1_MOUSE	Q02357 mus musculu
45	72.5	13.0	120	2	Q90XH5	Q90xh5 coturnix co

## ALIGNMENTS

### RESULT 1

#### UN5A\_HUMAN

ID UN5A\_HUMAN STANDARD; PRT; 842 AA.  
AC Q6ZN44; Q8TF26; Q96GP4;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).  
GN Name=UNC5A; Synonyms=KIAA1976, UNC5H1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Brain;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).

RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 302-842 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]  
RP SEQUENCE OF 624-728 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=21842142; PubMed=11853319;  
RA Nagase T., Kikuno R., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XXII.  
RT The complete sequences of 50 new cDNA clones which code for large

RT proteins.";  
RL DNA Res. 8:319-327(2001).  
RN [4]  
RP INDUCTION.  
RX PubMed=12598906; DOI=10.1038/ncb943;  
RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;  
RT "p53RDL1 regulates of p53-dependent apoptosis.";  
RL Nat. Cell Biol. 5:216-223(2003).  
RN [5]  
RP DOWN-REGULATION IN CANCER.  
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;  
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,  
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;  
RT "The netrin-1 receptors UNC5H are putative tumor suppressors  
controlling cell death commitment.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. It also acts as a dependence receptor required for  
CC apoptosis induction when not associated with netrin ligand.  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts  
CC with MAGED1. Interacts with PRKCABP, possibly mediating some  
CC interaction with PKC (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction  
CC with PRKCABP regulates its surface expression and leads to its  
CC removal from surface of neurons and growth cones (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1;  
CC IsoId=Q6ZN44-1; Sequence=Displayed;  
CC Note>No experimental confirmation available;  
CC Name=2;  
CC IsoId=Q6ZN44-2; Sequence=VSP\_011694, VSP\_011695;  
CC Note>No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q6ZN44-3; Sequence=VSP\_011693;  
CC Note>No experimental confirmation available;  
CC -!- INDUCTION: By p53/TP53.  
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which  
CC participates in the induction of apoptosis (By similarity).  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues.  
CC Phosphorylated by PKC in vitro (By similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis (By similarity).  
CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including  
CC colorectal, breast, ovary, uterus, stomach, lung, or kidney  
CC cancers.  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.

CC -!- CAUTION: Ref.3 sequence differs from that shown due to the  
 CC presence of introns.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; AK131380; BAD18531.1; -.  
 DR EMBL; BC009333; AAH09333.2; -.  
 DR EMBL; BC033727; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; AB075856; BAB85562.1; ALT\_SEQ.  
 DR Genew; HGNC:12567; UNC5A.  
 DR MIM; 607869; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR000884; TSP1.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00090; TSP\_1; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00209; TSP1; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 1.  
 KW Alternative splicing; Apoptosis; Developmental protein;  
 KW Immunoglobulin domain; Phosphorylation; Receptor; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 25 Potential.  
 FT CHAIN 26 842 Netrin receptor UNC5A.  
 FT DOMAIN 1 306 Extracellular (Potential).  
 FT TRANSMEM 307 327 Potential.  
 FT DOMAIN 328 842 Cytoplasmic (Potential).  
 FT DOMAIN 44 141 Ig-like.  
 FT DOMAIN 155 234 Ig-like C2-type.  
 FT DOMAIN 242 294 TSP type-1.  
 FT DOMAIN 439 542 ZU5.  
 FT DOMAIN 761 841 Death.  
 FT SITE 340 341 Cleavage (by caspase-3) (By similarity).  
 FT SITE 605 623 Interaction with DCC (By similarity).  
 FT DISULFID 65 124 By similarity.  
 FT DISULFID 170 221 By similarity.  
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 287 287 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 1 97 MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPD  
 LLPHFLVEPEDVYIVKKNKPVLLVCKAVPATQIFFKCNGEWV  
 RQVDHVIERSTDGSN -> MAGTSERSLISSISQPKAIECF  
 EVKKKAFLTHGRYHGSGATPPKTKDPKPETFCGQT (in  
 isoform 3).  
 FT /FTId=VSP\_011693.  
 FT VARSPLIC 296 301 TASGPE -> SESSLP (in isoform 2).  
 FT /FTId=VSP\_011694.  
 FT VARSPLIC 302 842 Missing (in isoform 2).  
 FT /FTId=VSP\_011695.

SQ SEQUENCE 842 AA; 92958 MW; 3DFADCF973131849 CRC64;  
 Query Match 100.0%; Score 559; DB 1; Length 842;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-52;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 TSNMTYGTNFNLLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
 |||||||  
 Db 439 TSNMTYGTNFNLLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 498  
  
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
 |||||||  
 Db 499 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 542

## RESULT 2

### UN5A\_MOUSE

ID UN5A\_MOUSE STANDARD; PRT; 898 AA.  
 AC Q8K1S4; Q6PEF7; Q80T71;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).  
 GN Name=Unc5a; Synonyms=Kiaa1976, Unc5h1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.  
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;  
 RA Engelkamp D.;  
 RT "Cloning of three mouse unc-5 genes and their expression patterns at  
 RT mid-gestation.";  
 RL Mech. Dev. 118:191-197(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Brain;  
 RX MEDLINE=22579291; PubMed=12693553;  
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,  
 RA Nakajima D., Nagase T., Ohara O., Koga H.;  
 RT "Prediction of the coding sequences of mouse homologues of KIAA gene:  
 RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous  
 RT cDNAs identified by screening of terminal sequences of cDNA clones  
 RT randomly sampled from size-fractionated libraries.";  
 RL DNA Res. 10:35-48(2003).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. It also acts as a dependence receptor required for  
CC apoptosis induction when not associated with netrin ligand (By  
CC similarity).  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts  
CC with MAGED1. Interacts with PRKCABP, possibly mediating some  
CC interaction with PKC (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction  
CC with PRKCABP regulates its surface expression and leads to its  
CC removal from surface of neurons and growth cones (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=1;  
CC IsoId=Q8K1S4-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q8K1S4-2; Sequence=VSP\_011697;  
CC Note>No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q8K1S4-3; Sequence=VSP\_011696;  
CC Note>No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.  
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which  
CC participates in the induction of apoptosis (By similarity).  
CC -!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic  
CC tyrosine residues (By similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis (By similarity).  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.  
CC -----  
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 CC -----  
 DR EMBL; AJ487852; CAD32250.1; -.  
 DR EMBL; AK122575; BAC65857.1; ALT\_INIT.  
 DR EMBL; BC058084; AAH58084.1; -.  
 DR HSSP; P07996; 1LSL.  
 DR MGD; MGI:894682; Unc5a.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR008085; TSP\_1.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00090; TSP\_1; 2.  
 DR Pfam; PF00791; ZU5; 1.  
 DR PRINTS; PR01705; TSP1REPEAT.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00209; TSP1; 2.  
 DR SMART; SM00218; ZU5; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Alternative splicing; Apoptosis; Developmental protein;  
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 25 Potential.  
 FT CHAIN 26 898 Netrin receptor UNC5A.  
 FT DOMAIN 26 361 Extracellular (Potential).  
 FT TRANSMEM 362 382 Potential.  
 FT DOMAIN 383 898 Cytoplasmic (Potential).  
 FT DOMAIN 44 141 Ig-like.  
 FT DOMAIN 155 234 Ig-like C2-type.  
 FT DOMAIN 242 296 TSP type-1 1.  
 FT DOMAIN 298 350 TSP type-1 2.  
 FT DOMAIN 495 598 ZU5.  
 FT DOMAIN 817 897 Death.  
 FT SITE 396 397 Cleavage (by caspase-3) (By similarity).  
 FT SITE 661 679 Interaction with DCC (By similarity).  
 FT DISULFID 65 124 By similarity.  
 FT DISULFID 170 221 By similarity.  
 FT CARBOHYD 107 107 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 218 218 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 343 343 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 1 790 Missing (in isoform 3).  
 FT VARSPLIC 241 296 /FTId=VSP\_011696.  
 FT VARSPLIC 241 296 Missing (in isoform 2).  
 FT VARSPLIC 241 296 /FTId=VSP\_011697.  
 FT CONFLICT 217 217 A -> P (in Ref. 3).  
 SQ SEQUENCE 898 AA; 98856 MW; 59F04BA2E196C1DB CRC64;

Query Match 99.1%; Score 554; DB 1; Length 898;  
 Best Local Similarity 99.0%; Pred. No. 2.9e-51;

Matches	103;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1 TSNMTYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60 								
Db	495 TSNMAYGTFNFLGGRLMIPNTGISLLIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 554								
Qy	61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104 								
Db	555 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 598								

RESULT 3

UN5A\_RAT

ID UN5A\_RAT STANDARD; PRT; 898 AA.  
AC 008721;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).  
GN Name=Unc5a; Synonyms=Unc5h1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Ventral spinal cord;  
RX MEDLINE=97271897; PubMed=9126742;  
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,  
RA Tessier-Lavigne M.;  
RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin  
RT receptors.";  
RL Nature 386:833-838(1997).  
RN [2]  
RP FUNCTION, AND INTERACTION WITH DCC.  
RX PubMed=10399920;  
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,  
RA Stein E.;  
RT "A ligand-gated association between cytoplasmic domains of UNC5 and  
RT DCC family receptors converts netrin-induced growth cone attraction to  
RT repulsion.";  
RL Cell 97:927-941(1999).  
RN [3]  
RP TISSUE SPECIFICITY.  
RX PubMed=11472849;  
RA Barrett C., Guthrie S.;  
RT "Expression patterns of the netrin receptor UNC5H1 among developing  
RT motor neurons in the embryonic rat hindbrain.";  
RL Mech. Dev. 106:163-166(2001).  
RN [4]  
RP FUNCTION.  
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;  
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;  
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";  
RL EMBO J. 20:2715-2722(2001).  
RN [5]

RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.  
RX PubMed=12598531; DOI=10.1074/jbc.M300415200;  
RA Williams M.E., Strickland P., Watanabe K., Hinck L.;  
RT "UNC5H1 induces apoptosis via its juxtamembrane region through an  
RT interaction with NRAGE.";  
RL J. Biol. Chem. 278:17483-17490(2003).  
RN [6]  
RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF  
RP 896-ALA--CYS-898.  
RX PubMed=14672991; DOI=23/36/11279;  
RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;  
RT "Surface expression of the netrin receptor UNC5H1 is regulated through  
RT a protein kinase C-interacting protein/protein kinase-dependent  
RT mechanism.";  
RL J. Neurosci. 23:11279-11288(2003).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. It also acts as a dependence receptor required for  
CC apoptosis induction when not associated with netrin ligand.  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts  
CC with MAGED1. Interacts with PRKCABP, possibly mediating some  
CC interaction with PKC.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction  
CC with PRKCABP regulates its surface expression and leads to its  
CC removal from surface of neurons and growth cones.  
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating  
CC neurons. Expressed at early stages of neural tube development in  
CC the ventral spinal cord. In developing hindbrain, it colocalizes  
CC with a number of cranial motor neuron subpopulations from  
CC embryonic E11 to E14, while DCC is expressed by motor neurons at  
CC E12. Also expressed in non-neuronal structures, such as the basal  
CC plane of the hindbrain and midbrain, in the developing  
CC hypothalamus, thalamus and in the pallidium.  
CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which  
CC participates in the induction of apoptosis.  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
CC similarity). Phosphorylated by PKC in vitro.  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis.  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.  
CC -----  
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## RESULT 4

## UN5C\_MOUSE

ID UN5C\_MOUSE STANDARD; PRT; 931 AA.  
AC 008747; Q8CD16;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)  
DE (Rostral cerebellar malformation protein).  
GN Name=Unc5c; Synonyms=Rcm, Unc5h3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, DISEASE, AND TISSUE  
SPECIFICITY.  
RC STRAIN=C57B6/SJL;  
RX MEDLINE=97271898; PubMed=9126743;  
RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,  
RA Knowles B.B.;  
RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like  
protein.";  
RL Nature 386:838-842(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [3]  
RP FUNCTION, AND TISSUE SPECIFICITY.  
RX PubMed=9389662;  
RA Przyborski S.A., Knowles B.B., Ackerman S.L.;  
RT "Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion  
RT during the formation of the rostral cerebellar boundary.";  
RL Development 125:41-50(1998).  
RN [4]  
RP INTERACTION WITH DCC.  
RX PubMed=10399920;  
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,  
RA Stein E.;  
RT "A ligand-gated association between cytoplasmic domains of UNC5 and  
RT DCC family receptors converts netrin-induced growth cone attraction to  
RT repulsion.";  
RL Cell 97:927-941(1999).  
RN [5]  
RP PHOSPHORYLATION SITE TYR-568, AND MUTAGENESIS OF TYR-568.  
RX PubMed=11533026; DOI=10.1074/jbc.M103872200;  
RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;  
RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of  
RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";  
RL J. Biol. Chem. 276:40917-40925(2001).  
RN [6]  
RP FUNCTION.  
RX PubMed=12451134; DOI=22/23/10346;  
RA Finger J.H., Bronson R.T., Harris B., Johnson K., Przyborski S.A.,  
RA Ackerman S.L.;  
RT "The netrin 1 receptors Unc5h3 and Dcc are necessary at multiple  
RT choice points for the guidance of corticospinal tract axons.";  
RL J. Neurosci. 22:10346-10356(2002).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. Also involved in corticospinal tract axon guidances  
CC independently of DCC. It also acts as a dependence receptor  
CC required for apoptosis induction when not associated with netrin  
CC ligand.  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=O08747-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=O08747-2; Sequence=VSP\_011702;  
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating  
CC neurons. Highly expressed in brain and lung. Weakly expressed in  
CC testis, ovary, spleen, thymus and bladder. Expressed at very low  
CC level in kidney, intestine and salivary gland.  
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.  
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11  
CC phosphatase, suggesting that its activity is regulated by

CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is  
CC netrin-dependent.  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis (By similarity).  
CC -!- DISEASE: Defects in Unc5c are the cause of rostral cerebellar  
CC malformation (Rcm). Rcm is characterized by cerebellar and  
CC midbrain defects, apparently as a result of abnormal neuronal  
CC migration.  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.  
CC -----  
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CC -----  
DR EMBL; U72634; AAB54103.1; -.  
DR EMBL; AK031655; BAC27495.1; -.  
DR HSSP; P07996; 1LSL.  
DR MGD; MGI:1095412; Unc5c.  
DR GO; GO:0005886; C:plasma membrane; IC.  
DR GO; GO:0005042; F:netrin receptor activity; IDA.  
DR GO; GO:0005515; F:protein binding; IDA.  
DR GO; GO:0007420; P:brain development; IMP.  
DR GO; GO:0030334; P:regulation of cell migration; IMP.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH\_like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR008085; TSP\_1.  
DR InterPro; IPR000906; ZU5.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00090; TSP\_1; 2.  
DR Pfam; PF00791; ZU5; 1.  
DR PRINTS; PR01705; TSP1REPEAT.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00209; TSP1; 2.  
DR SMART; SM00218; ZU5; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS50092; TSP1; 2.  
KW Alternative splicing; Apoptosis; Developmental protein;  
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 40 Potential.

FT CHAIN 41 931 Netrin receptor UNC5C.  
 FT DOMAIN 41 380 Extracellular (Potential).  
 FT TRANSMEM 381 401 Potential.  
 FT DOMAIN 402 931 Cytoplasmic (Potential).  
 FT DOMAIN 62 159 Ig-like.  
 FT DOMAIN 161 256 Ig-like C2-type.  
 FT DOMAIN 260 314 TSP type-1 1.  
 FT DOMAIN 316 368 TSP type-1 2.  
 FT DOMAIN 528 631 ZU5.  
 FT DOMAIN 850 929 Death.  
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).  
 FT SITE 694 712 Interaction with DCC (By similarity).  
 FT DISULFID 83 142 By similarity.  
 FT DISULFID 188 239 By similarity.  
 FT MOD\_RES 568 568 Phosphotyrosine.  
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 370 370 A -> GFIYPISTEHRPQNEYGFSS (in isoform 2).  
 /FTId=VSP\_011702.  
 FT MUTAGEN 568 568 Y->F: Abolishes interaction with PTPN11,  
 leading to a increased level of  
 phosphorylation.  
 FT CONFLICT 16 16 L -> I (in Ref. 2).  
 FT CONFLICT 733 733 H -> R (in Ref. 2).  
 FT CONFLICT 924 924 S -> Y (in Ref. 2).  
 SQ SEQUENCE 931 AA; 103062 MW; 8A5D951A4EECA179 CRC64;

Query Match 62.3%; Score 348; DB 1; Length 931;  
 Best Local Similarity 58.6%; Pred. No. 7.6e-29;  
 Matches 58; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIIPPDAIPRGKIEIYLTLHKPEDVRLPLAGCQTLLSPIV 65  
 :||||| |||| |:|||||:||||| |||||:|||||:|||: ||::| |: |||||:|||:  
 Db 533 FGTFNSLGGHIIIPNSGVSLIIPAGAIIPQGRVYEMYVTVHRKENMRPPMEDSQTLTPVV 592  
 Qy 66 SCGPPGVLLTRPVILAMDHCGEPSPDWSLRLKKQSCEG 104  
 ||||||| ||||||||| : || ::|| : | ::|| |: :|  
 Db 593 SCGPPGALLTRPVILTLHHCADPSTEDWKIQLKNQAVQG 631

**RESULT 5**  
**UN5C\_CHICK**  
 ID UN5C\_CHICK STANDARD; PRT; 931 AA.  
 AC Q7T2Z5;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)  
 DE (cUNC-5H3).  
 GN Name=UNC5C;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RX PubMed=12799087;  
RA Guan W., Condic M.L.;  
RT "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during  
RT chick dorsal root ganglia development.";  
RL Gene Expr. Patterns 3:369-373(2003).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- TISSUE SPECIFICITY: Restricted to proprioceptive neurons.  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.  
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CC -----  
DR EMBL; AY187310; AAO67275.1; -.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR000906; ZU5.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00090; TSP\_1; 2.  
DR Pfam; PF00791; ZU5; 1.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00209; TSP1; 2.  
DR SMART; SM00218; ZU5; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS50092; TSP1; 2.  
KW Developmental protein; Immunoglobulin domain; Phosphorylation;  
KW Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 39 Potential.  
FT CHAIN 40 931 Netrin receptor UNC5C.  
FT DOMAIN 40 380 Extracellular (Potential).  
FT TRANSMEM 381 401 Potential.  
FT DOMAIN 402 931 Cytoplasmic (Potential).  
FT DOMAIN 62 159 Ig-like.  
FT DOMAIN 161 256 Ig-like C2-type.  
FT DOMAIN 260 314 TSP type-1 1.  
FT DOMAIN 316 368 TSP type-1 2.  
FT DOMAIN 528 631 ZU5.  
FT DOMAIN 850 929 Death.

FT DISULFID 83 142 By similarity.  
 FT DISULFID 188 239 By similarity.  
 FT CARBOHYD 236 236 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 361 361 N-linked (GlcNAc . . .) (Potential).  
 SQ SEQUENCE 931 AA; 102906 MW; 1E23A0D84F2E2C62 CRC64;  
  
 Query Match 61.9%; Score 346; DB 1; Length 931;  
 Best Local Similarity 58.6%; Pred. No. 1.3e-28;  
 Matches 58; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIPDAIPRGKIYIYLTLHKPEDVRLPLAGCQTLSPIV 65  
 :||||| |||| |:|||||:||| | :|||:||:||:| :| |:| :| ||||:||:  
 Db 533 FGTFNSLGGHLVIPNSGVSLIPAGAVPQGRVYEMYVTVHRKEGMRPPVEDSQTLLTPVV 592  
  
 Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 104  
 ||||||| |||||||:| | || ||:| | | :|| |: :|  
 Db 593 SCGPPGALLTRPVVLTMHCAEPNMDDWQIQLKHQAGQG 631

**RESULT 6**  
**UN5C\_RAT**  
 ID UN5C\_RAT STANDARD; PRT; 931 AA.  
 AC Q761X5;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).  
 GN Name=Unc5c; Synonyms=Unc5h3;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND DISEASE.  
 RX PubMed=15010202; DOI=10.1016/j.molbrainres.2003.12.003;  
 RA Kuramoto T., Kuwamura M., Serikawa T.;  
 RT "Rat neurological mutations cerebellar vermis defect and hobble are  
 caused by mutations in the netrin-1 receptor gene Unc5h3.";  
 RL Brain Res. Mol. Brain Res. 122:103-108(2004).  
 RN [2]  
 RP FUNCTION.  
 RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;  
 RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;  
 RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";  
 RL EMBO J. 20:2715-2722(2001).  
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
 CC axon repulsion of neuronal growth cones in the developing nervous  
 CC system upon ligand binding. Axon repulsion in growth cones may be  
 CC caused by its association with DCC that may trigger signaling for  
 CC repulsion. Also involved in corticospinal tract axon guidances  
 CC independently of DCC. It also acts as a dependence receptor  
 CC required for apoptosis induction when not associated with netrin  
 CC ligand.  
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in

CC kidney. Not expressed in developing or adult lung.  
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.  
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11  
CC phosphatase, suggesting that its activity is regulated by  
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is  
CC netrin-dependent (By similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis.  
CC -!- DISEASE: Defects in Unc5c are the cause of cerebellar vermis  
CC defect (cvd) and hobble (hob) phenotypes. Cvd and hob rats exhibit  
CC cerebellar and midbrain defects, possibly as a result of abnormal  
CC neuronal migration, and exhibit laminar structure abnormalities in  
CC the fused cerebellar hemispheres and ectopic cerebellar tissues in  
CC the cerebello-pontine junction.  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----

DR EMBL; AB118026; BAD05181.1; -.  
DR RGD; 735109; Unc5c.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH\_like.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR000885; TSP\_1.  
DR InterPro; IPR000906; ZU5.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00090; TSP\_1; 2.  
DR Pfam; PF00791; ZU5; 1.  
DR PRINTS; PR01705; TSP1REPEAT.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00209; TSP1; 2.  
DR SMART; SM00218; ZU5; 1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
DR PROSITE; PS50092; TSP1; 2.  
KW Apoptosis; Developmental protein; Immunoglobulin domain;  
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 40 Potential.

FT CHAIN 41 931 Netrin receptor UNC5C.  
 FT DOMAIN 41 380 Extracellular (Potential).  
 FT TRANSMEM 381 401 Potential.  
 FT DOMAIN 402 931 Cytoplasmic (Potential).  
 FT DOMAIN 62 159 Ig-like.  
 FT DOMAIN 161 256 Ig-like C2-type.  
 FT DOMAIN 260 314 TSP type-1 1.  
 FT DOMAIN 316 368 TSP type-1 2.  
 FT DOMAIN 528 631 ZU5.  
 FT DOMAIN 850 929 Death.  
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).  
 FT SITE 694 712 Interaction with DCC (By similarity).  
 FT DISULFID 83 142 By similarity.  
 FT DISULFID 188 239 By similarity.  
 FT MOD\_RES 568 568 Phosphotyrosine (By similarity).  
 FT CARBOHYD 236 236 N-linked (GlcNAc . . .) (Potential).  
 FT CARBOHYD 361 361 N-linked (GlcNAc . . .) (Potential).  
 SQ SEQUENCE 931 AA; 103134 MW; 25B183A97BCB8401 CRC64;

Query Match 61.7%; Score 345; DB 1; Length 931;  
 Best Local Similarity 57.6%; Pred. No. 1.6e-28;  
 Matches 57; Conservative 24; Mismatches 18; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMPINTGISLLIPDAIPRGKIFYEYLTLHKPEDVRLPLAGCQTLSPIV 65  
 :||||| ||| |:|||:||:||||| |||:||::||:||:||:| :| :|||:||:|  
 Db 533 FGTFNLSLGGHLIIPNSGVSLI PAGAI PQGRVYEMYTVHRKENMRPPMEDSQTLTPVV 592  
 Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRLKKQSCEG 104  
 ||||||| ||||||||| : |||:||: :| :||| |: :|  
 Db 593 SCGPPGALLTRPVILTLHHCADPNTEDWKIQLKNQAVQG 631

## RESULT 7

### UN5C\_HUMAN

ID UN5C\_HUMAN STANDARD; PRT; 931 AA.  
 AC O95185; Q8IUT0;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).  
 GN Name=UNC5C; Synonyms=UNC5H3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.  
 RC TISSUE=Brain;  
 RX MEDLINE=99000841; PubMed=9782087; DOI=10.1006/geno.1998.5425;  
 RA Ackerman S.L., Knowles B.B.;  
 RT "Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23.";  
 RL Genomics 52:205-208(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP DOWN-REGULATION IN CANCER.  
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;  
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,  
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;  
RT "The netrin-1 receptors UNC5H are putative tumor suppressors  
RT controlling cell death commitment.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. Also involved in corticospinal tract axon guidances  
CC independently of DCC. It also acts as a dependence receptor  
CC required for apoptosis induction when not associated with netrin  
CC ligand (By similarity).  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=095185-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=095185-2; Sequence=VSP\_011700, VSP\_011701;  
CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in  
CC kidney. Not expressed in developing or adult lung.  
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.  
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11  
CC phosphatase, suggesting that its activity is regulated by  
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is  
CC netrin-dependent (By similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis (By similarity).  
CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including  
CC colorectal, breast, ovary, uterus, stomach, lung, or kidney

CC           cancers.

CC    -!- SIMILARITY: Belongs to the UNC-5 family.

CC    -!- SIMILARITY: Contains 1 death domain.

CC    -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC    -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC    -!- SIMILARITY: Contains 2 TSP type-1 domains.

CC    -!- SIMILARITY: Contains 1 ZU5 domain.

CC

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DR       EMBL; AF055634; AAC67491.1; -.

DR       EMBL; BC041156; AAH41156.1; -.

DR       HSSP; P07996; 1LSL.

DR       Genew; HGNC:12569; UNC5C.

DR       MIM; 603610; -.

DR       GO; GO:0005042; F:netrin receptor activity; TAS.

DR       GO; GO:0007411; P:axon guidance; TAS.

DR       GO; GO:0007420; P:brain development; TAS.

DR       InterPro; IPR000488; Death.

DR       InterPro; IPR011029; DEATH\_like.

DR       InterPro; IPR007110; Ig-like.

DR       InterPro; IPR003598; Ig\_c2.

DR       InterPro; IPR000884; TSP1.

DR       InterPro; IPR008085; TSP\_1.

DR       InterPro; IPR000906; ZU5.

DR       Pfam; PF00531; Death; 1.

DR       Pfam; PF00047; ig; 1.

DR       Pfam; PF00090; TSP\_1; 2.

DR       Pfam; PF00791; ZU5; 1.

DR       PRINTS; PR01705; TSP1REPEAT.

DR       SMART; SM00005; DEATH; 1.

DR       SMART; SM00408; IGc2; 1.

DR       SMART; SM00209; TSP1; 2.

DR       SMART; SM00218; ZU5; 1.

DR       PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.

DR       PROSITE; PS50835; IG\_LIKE; 1.

DR       PROSITE; PS50092; TSP1; 2.

KW       Alternative splicing; Apoptosis; Developmental protein;

KW       Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;

KW       Repeat; Signal; Transmembrane.

FT       SIGNAL       1       40       Potential.

FT       CHAIN        41       931      Netrin receptor UNC5C.

FT       DOMAIN       41       380      Extracellular (Potential).

FT       TRANSMEM     381       401      Potential.

FT       DOMAIN       402       931      Cytoplasmic (Potential).

FT       DOMAIN       62       159      Ig-like.

FT       DOMAIN       161       256      Ig-like C2-type.

FT       DOMAIN       260       314      TSP type-1 1.

FT       DOMAIN       316       368      TSP type-1 2.

FT       DOMAIN       528       631      ZU5.

FT       DOMAIN       850       929      Death.

FT SITE 415 416 Cleavage (by caspase-3) (By similarity).  
 FT SITE 694 712 Interaction with DCC (By similarity).  
 FT DISULFID 83 142 By similarity.  
 FT DISULFID 188 239 By similarity.  
 FT MOD\_RES 568 568 Phosphotyrosine (By similarity).  
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 370 370 T -> SFIYPISTEQRTQNEYGFSS (in isoform 2).  
 /FTId=VSP\_011700.  
 FT VARSPLIC 579 931 Missing (in isoform 2).  
 /FTId=VSP\_011701.  
 FT VARIANT 37 37 G -> V (in dbSNP:2306715).  
 /FTId=VAR\_019731.  
 FT VARIANT 721 721 T -> M (in dbSNP:2289043).  
 /FTId=VAR\_019732.  
 FT CONFLICT 219 219 T -> I (in Ref. 1).  
 FT CONFLICT 489 489 S -> T (in Ref. 1).  
 SQ SEQUENCE 931 AA; 103101 MW; EFD71122C98DABB8 CRC64;

Query Match 60.3%; Score 337; DB 1; Length 931;  
 Best Local Similarity 55.6%; Pred. No. 1.2e-27;  
 Matches 55; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

Qy 6 YGTFNFLGGRLMIPNTGISLLIPPDAAIPRGKIEIYLTLHKPEDVRLPLAGCQTLLSPIV 65  
 ::|| ||| |::||| :||| ||| :||:||:||:||:| :| |:| |:| ||||:||:  
 Db 533 FGSFNSLGGHLIVPNNSGVSSLIPAGAIPQGRVYEMYVTVHRKETMRPPMDDSQTLTPVV 592  
 Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSWSLRKKQSCEG 104  
 ||||||| |||||||:| | || :|: :| :|| |: :|  
 Db 593 SCGPPGALLTRPVVLTMHHCADPNTEDWKILLKNQAAQG 631

## RESULT 8

### UN5B\_XENLA

ID UN5B\_XENLA STANDARD; PRT; 943 AA.  
 AC Q8JGT4;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5B precursor (UNC-5 homolog) (Protein XUNC-5).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RX MEDLINE=22239703; PubMed=12351179; DOI=10.1016/S0925-4773(02)00215-0;  
 RA Anderson R.B., Holt C.E.;  
 RT "Expression of UNC-5 in the developing Xenopus visual system.";  
 RL Mech. Dev. 118:157-160(2002).  
 CC --!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
 CC axon repulsion of neuronal growth cones in the developing nervous  
 CC system upon ligand binding (By similarity).  
 CC --!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC --!- TISSUE SPECIFICITY: In the developing visual system, it is  
 CC expressed within the developing optic vesicles and later become

CC restricted to the dorsal ciliary marginal zone, a site of  
 CC retinoblast proliferation and differentiation.  
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the UNC-5 family.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
 CC -!- SIMILARITY: Contains 1 ZU5 domain.  
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 CC -----  
 DR EMBL; AY099459; AAM34486.1; -.  
 DR HSSP; P07996; 1LSL.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR008085; TSP\_1.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00090; TSP\_1; 2.  
 DR Pfam; PF00791; ZU5; 1.  
 DR PRINTS; PR01705; TSP1REPEAT.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00408; IGc2; 1.  
 DR SMART; SM00209; TSP1; 2.  
 DR SMART; SM00218; ZU5; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;  
 KW Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 30 Potential.  
 FT CHAIN 31 943 Netrin receptor UNC5B.  
 FT DOMAIN 31 380 Extracellular (Potential).  
 FT TRANSMEM 381 401 Potential.  
 FT DOMAIN 402 943 Cytoplasmic (Potential).  
 FT DOMAIN 51 148 Ig-like.  
 FT DOMAIN 150 245 Ig-like C2-type.  
 FT DOMAIN 249 303 TSP type-1 1.  
 FT DOMAIN 305 357 TSP type-1 2.  
 FT DOMAIN 540 643 ZU5.  
 FT DOMAIN 863 941 Death.  
 FT DISULFID 72 131 By similarity.  
 FT DISULFID 177 228 By similarity.  
 FT CARBOHYD 225 225 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 350 350 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;  
 Query Match 55.3%; Score 309; DB 1; Length 943;  
 Best Local Similarity 55.8%; Pred. No. 1.3e-24;  
 Matches 58; Conservative 17; Mismatches 29; Indels 0; Gaps 0;  
  
 QY 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIEIYLTLHKPEDVRLPLAGCQTL 60  
 :||| |||| |||||| ||||:||||| ||||:|| ||:|| ::| |: || | ||:  
 Db 540 SSNSVTGTFGSLLGGLTFPNTGVSLIPQGAIPQGKYYEMYLMINKRENTVLPSEGQT 599  
  
 QY 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
 ||||:||| :||| :||| : || : | |::| || :|:  
 Db 600 LSPIITCGPTGLLLCKPVILTVPHCADINTSDWILQLKTQSHQG 643

## RESULT 9

### UN5B\_HUMAN

ID UN5B\_HUMAN STANDARD; PRT; 945 AA.  
 AC Q8IZJ1; Q86SN3; Q8N1Y2; Q9H9F3;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2)  
 DE (p53-regulated receptor for death and life protein 1)  
 DE (UNQ1883/PRO4326).  
 GN Name=UNC5B; Synonyms=P53RDL1, UNC5H2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION  
 RP WITH GNAI2.  
 RC TISSUE=Lung;  
 RX MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;  
 RA Komatsuzaki K., Dalvin S., Kinane T.B.;  
 RT "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule  
 RT UNC5H2.";  
 RL Biochem. Biophys. Res. Commun. 297:898-905(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND MUTAGENESIS OF ASP-412.  
 RX PubMed=12598906; DOI=10.1038/ncb943;  
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;  
 RT "p53RDL1 regulates of p53-dependent apoptosis.";  
 RL Nat. Cell Biol. 5:216-223(2003).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.;

RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [4]  
RP SEQUENCE OF 361-945 FROM N.A.  
RC TISSUE=Amygdala, and Teratocarcinoma;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
RN [5]  
RP DOWN-REGULATION IN CANCER.  
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;  
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,  
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;  
RT "The netrin-1 receptors UNC5H are putative tumor suppressors  
controlling cell death commitment.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. It also acts as a dependence receptor required for  
CC apoptosis induction when not associated with netrin ligand.  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By  
CC similarity). Interacts with GNAI2 via its cytoplasmic part.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q8IZJ1-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q8IZJ1-2; Sequence=VSP\_011698;  
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed at  
CC lower level in developing lung, cartilage, kidney and  
CC hematopoietic and immune tissues.  
CC -!- INDUCTION: By p53/TP53.  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
CC similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis.  
CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including  
CC colorectal, breast, ovary, uterus, stomach, lung, or kidney  
CC cancers.  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; AY126437; AAM95701.1; -.  
DR EMBL; AB096256; BAC57998.1; -.  
DR EMBL; AY358351; AAQ88717.1; -.  
DR EMBL; AK022859; BAB14276.1; ALT\_INIT.  
DR EMBL; AK094595; BAC04382.1; ALT\_INIT.  
DR HSSP; P07996; 1LSL.  
DR Genew; HGNC:12568; UNC5B.  
DR MIM; 607870; -.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH\_like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR008085; TSP\_1.  
DR InterPro; IPR000906; ZU5.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00090; TSP\_1; 2.  
DR Pfam; PF00791; ZU5; 1.  
DR PRINTS; PR01705; TSP1REPEAT.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00209; TSP1; 2.  
DR SMART; SM00218; ZU5; 1.

DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Alternative splicing; Apoptosis; Developmental protein;  
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;  
 KW Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 945 Netrin receptor UNC5B.  
 FT DOMAIN 27 377 Extracellular (Potential).  
 FT TRANSMEM 378 398 Potential.  
 FT DOMAIN 399 945 Cytoplasmic (Potential).  
 FT DOMAIN 48 145 Ig-like.  
 FT DOMAIN 147 242 Ig-like C2-type.  
 FT DOMAIN 246 300 TSP type-1 1.  
 FT DOMAIN 302 354 TSP type-1 2.  
 FT DOMAIN 541 644 ZU5.  
 FT DOMAIN 865 943 Death.  
 FT SITE 412 413 Cleavage (by caspase-3).  
 FT SITE 707 725 Interaction with DCC (By similarity).  
 FT DISULFID 69 128 By similarity.  
 FT DISULFID 174 225 By similarity.  
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 356 367 NKKTLSDPNSHL -> M (in isoform 2).  
 FT /FTId=VSP\_011698.  
 FT VARIANT 516 516 A -> T (in dbSNP:10509332).  
 FT /FTId=VAR\_019730.  
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and  
 subsequent induction of apoptosis.  
 FT CONFLICT 483 483 K -> E (in Ref. 3).  
 FT CONFLICT 851 851 L -> P (in Ref. 3; BAB14276).  
 SQ SEQUENCE 945 AA; 103637 MW; 56064E335F323447 CRC64;

Query Match 51.3%; Score 287; DB 1; Length 945;  
 Best Local Similarity 58.6%; Pred. No. 3.3e-22;  
 Matches 58; Conservative 13; Mismatches 26; Indels 2; Gaps 2;

Qy 7 GTFNFLGGRLMIPNTGISLLIPPPDAIPRGKYEIYLTLHKPEDVRLPLA-GCQTLLSPIV 65  
 ||| ||||| || ||::|||:| ||||:|| ||:|| ::|| | |||: | ||:||| |  
 Db 547 GTFGCLGGRLSIPGTGVSLVPNGAIPQGKFYEMYLLINKAEST-LPLSEGTQTVLSPSV 605

Qy 66 SCGPPGVLLTRPVILAMDHCGEPS PDSW SRLKKQSCEG 104  
 :||| |:||| ||||| || ||| | | :|| |: :|  
 Db 606 TCGPTGLLCRPVILTMPHCAEV SARDWIFQLKTQAHQG 644

## RESULT 10

### UN5B\_RAT

ID UN5B\_RAT STANDARD; PRT; 945 AA.  
 AC O08722;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).  
 GN Name=Unc5b; Synonyms=Unc5h2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE  
SPECIFICITY.  
RX MEDLINE=97271897; PubMed=9126742;  
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,  
RA Tessier-Lavigne M.;  
RT "Vertebrate homologues of *C. elegans* UNC-5 are candidate netrin  
receptors.";  
RL Nature 386:833-838(1997).  
RN [2]  
RP FUNCTION, AND INTERACTION WITH DCC.  
RX PubMed=10399920;  
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,  
RA Stein E.;  
RT "A ligand-gated association between cytoplasmic domains of UNC5 and  
RT DCC family receptors converts netrin-induced growth cone attraction to  
RT repulsion.";  
RL Cell 97:927-941(1999).  
RN [3]  
RP FUNCTION, AND MUTAGENESIS OF ASP-412.  
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;  
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;  
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";  
RL EMBO J. 20:2715-2722(2001).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. It also acts as a dependence receptor required for  
CC apoptosis induction when not associated with netrin ligand.  
CC -!- SUBUNIT: Interacts with GNAI2 via its cytoplasmic part (By  
CC similarity). Interacts with the cytoplasmic part of DCC.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating  
CC neurons. Expressed in the developing sensory ganglia that flank  
CC the spinal cord from E12, peaking at E14. Expressed in the roof  
CC plate region of the spinal cord from E14.  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
CC similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis.  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.  
CC -----  
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 CC -----  
 DR EMBL; U87306; AAB57679.1; -.  
 DR HSSP; P07996; 1LSL.  
 DR RGD; 621756; Unc5h2.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR008085; TSP\_1.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00090; TSP\_1; 2.  
 DR Pfam; PF00791; ZU5; 1.  
 DR PRINTS; PR01705; TSP1REPEAT.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00408; IGc2; 1.  
 DR SMART; SM00209; TSP1; 2.  
 DR SMART; SM00218; ZU5; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Apoptosis; Developmental protein; Immunoglobulin domain;  
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 945 Netrin receptor UNC5B.  
 FT DOMAIN 27 377 Extracellular (Potential).  
 FT TRANSMEM 378 398 Potential.  
 FT DOMAIN 399 945 Cytoplasmic (Potential).  
 FT DOMAIN 48 145 Ig-like.  
 FT DOMAIN 153 242 Ig-like C2-type.  
 FT DOMAIN 246 300 TSP type-1 1.  
 FT DOMAIN 302 354 TSP type-1 2.  
 FT DOMAIN 541 644 ZU5.  
 FT DOMAIN 865 943 Death.  
 FT SITE 412 413 Cleavage (by caspase-3).  
 FT SITE 707 725 Interaction with DCC.  
 FT DISULFID 69 128 By similarity.  
 FT DISULFID 174 225 By similarity.  
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).  
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and  
     subsequent induction of apoptosis.  
 SQ SEQUENCE 945 AA; 103520 MW; 6E9C2A262E560B9B CRC64;  
  
 Query Match                 49.6%; Score 277; DB 1; Length 945;  
 Best Local Similarity     52.9%; Pred. No. 4.1e-21;  
 Matches   55; Conservative 17; Mismatches 30; Indels 2; Gaps 2;  
  
 QY                 2 SNMTYGTFNFLGGRLMIPNTGISLLIPPPDAIPRGKIYEIYLTLHKPEDVRLPLA-GCQTL 60  
 . :    |||    ||||| || |||:|||    |||:|||    ||:|||    ::|||    |||:    |||:  
 Db                 542 SSSVSGTGFGLGGRLTIPGTGVSLVPNGAIHQGKFYDLYLRINKTEST-LPLSEGSQTV 600  
  
 Qy                 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104

||| |:||| |:|| |||:| : ||| | :||| |: :|  
Db 601 LSPSVTCGPTGLLCRPVVLTVPHCAEVIAVDWIFQLKTQAHQG 644

RESULT 11  
UN5B\_MOUSE  
ID UN5B\_MOUSE STANDARD; PRT; 945 AA.  
AC Q8K1S3; Q6PFH0; Q80Y85; Q9D398;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).  
GN Name=Unc5b; Synonyms=Unc5h2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.  
RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;  
RA Engelkamp D.;  
RT "Cloning of three mouse unc-5 genes and their expression patterns at  
RT mid-gestation.";  
RL Mech. Dev. 118:191-197(2002).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).

RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP TISSUE SPECIFICITY.  
RX PubMed=12799072;  
RA Dalvin S., Anselmo M.A., Prodhan P., Komatsuzaki K., Schnitzer J.J.,  
RA Kinane T.B.;  
RT "Expression of Netrin-1 and its two receptors DCC and UNC5H2 in the  
RT developing mouse lung.";  
RL Gene Expr. Patterns 3:279-283(2003).  
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates  
CC axon repulsion of neuronal growth cones in the developing nervous  
CC system upon ligand binding. Axon repulsion in growth cones may be  
CC caused by its association with DCC that may trigger signaling for  
CC repulsion. It also acts as a dependence receptor required for  
CC apoptosis induction when not associated with netrin ligand (By  
CC similarity).  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts  
CC with GNAI2 via its cytoplasmic part (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q8K1S3-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q8K1S3-2; Sequence=VSP\_011699;  
CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Expressed in lung  
CC during late development. Expressed during early blood vessel  
CC formation, in the semicircular canal and in a dorsal to ventral  
CC gradient in the retina.  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
CC similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce

CC apoptosis (By similarity).  
 CC -!- SIMILARITY: Belongs to the UNC-5 family.  
 CC -!- SIMILARITY: Contains 1 death domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
 CC -!- SIMILARITY: Contains 1 ZU5 domain.  
 CC -----  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; AJ487853; CAD32251.1; -.  
 DR EMBL; AK018177; BAB31108.1; -.  
 DR EMBL; BC048162; AAH48162.1; ALT\_INIT.  
 DR EMBL; BC057560; AAH57560.1; -.  
 DR HSSP; P07996; ILSL.  
 DR MGD; MGI:894703; Unc5b.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR008085; TSP\_1.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00090; TSP\_1; 2.  
 DR Pfam; PF00791; ZU5; 1.  
 DR PRINTS; PR01705; TSP1REPEAT.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00408; IGc2; 1.  
 DR SMART; SM00209; TSP1; 2.  
 DR SMART; SM00218; ZU5; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Alternative splicing; Apoptosis; Developmental protein;  
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 26 Potential.  
 FT CHAIN 27 945 Netrin receptor UNC5B.  
 FT DOMAIN 27 377 Extracellular (Potential).  
 FT TRANSMEM 378 398 Potential.  
 FT DOMAIN 399 945 Cytoplasmic (Potential).  
 FT DOMAIN 48 145 Ig-like.  
 FT DOMAIN 153 242 Ig-like C2-type.  
 FT DOMAIN 246 300 TSP type-1 1.  
 FT DOMAIN 302 354 TSP type-1 2.  
 FT DOMAIN 541 644 ZU5.  
 FT DOMAIN 865 943 Death.  
 FT SITE 412 413 Cleavage (by caspase-3) (By similarity).  
 FT SITE 707 725 Interaction with DCC (By similarity).

FT DISULFID 69 128 By similarity.  
 FT DISULFID 174 225 By similarity.  
 FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 356 367 NQRTLNDPKSHP -> T (in isoform 2).  
 /FTId=VSP\_011699.  
 FT CONFLICT 238 238 T -> A (in Ref. 2).  
 FT CONFLICT 394 394 V -> E (in Ref. 2).  
 FT CONFLICT 679 679 T -> S (in Ref. 2).  
 FT CONFLICT 874 874 N -> D (in Ref. 2).  
 SQ SEQUENCE 945 AA; 103738 MW;. 80E896F0F0E06012 CRC64;  
  
 Query Match 49.0%; Score 274; DB 1; Length 945;  
 Best Local Similarity 51.9%; Pred. No. 8.6e-21;  
 Matches 54; Conservative 18; Mismatches 30; Indels 2; Gaps 2;  
  
 Qy 2 SNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIVYEIYLTLHKPEDVRLPLA-GCQTL 60  
 |: ||| |||| :| ||:|||:| ||||:|| |::|| ::|| | |||: | ||:  
 Db 542 SSSVSGTGFGLGGRLSLPGTVSLLVPNGAIPQGKFYDLYLHINKAEST-LPLSEGSQTV 600  
  
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRLKKQSCEG 104  
 ||| |:||| |:|| |||:| :|| | | :|| | :|| | :|  
 Db 601 LSPSVTCGPTGLLLCPVVLTVPHCAEVIAQGDWIFQLKTQAHQG 644

RESULT 12  
 UN5D\_MOUSE  
 ID UN5D\_MOUSE STANDARD; PRT; 956 AA.  
 AC Q8K1S2;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4).  
 GN Name=Unc5d; Synonyms=Unc5h4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;  
 RA Engelkamp D.;  
 RT "Cloning of three mouse Unc5 genes and their expression patterns at  
 mid-gestation.";  
 RL Mech. Dev. 118:191-197(2002).  
 CC -!- FUNCTION: Receptor for netrin involved in cell migration. May be  
 involved in axon guidance by mediating axon repulsion of neuronal  
 growth cones in the developing nervous system upon ligand binding.  
 CC Axon repulsion in growth cones may be caused by its association  
 with DCC that may trigger signaling for repulsion. It also acts as  
 a dependence receptor required for apoptosis induction when not  
 associated with netrin ligand (By similarity).  
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
 CC -!- TISSUE SPECIFICITY: Expressed in developing limb and mammary  
 gland.

CC --!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By similarity).  
 CC --!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleavage does not take place when the receptor is associated with netrin ligand. Its cleavage by caspases is required to induce apoptosis (By similarity).  
 CC --!- SIMILARITY: Belongs to the UNC-5 family.  
 CC --!- SIMILARITY: Contains 1 death domain.  
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
 CC --!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC --!- SIMILARITY: Contains 2 TSP type-1 domains.  
 CC --!- SIMILARITY: Contains 1 ZU5 domain.  
 CC -----  
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 CC -----  
 DR EMBL; AJ487854; CAD32252.1; -.  
 DR HSSP; P07996; 1LSL.  
 DR MGD; MGI:2389364; Unc5d.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR008085; TSP\_1.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00531; Death; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR Pfam; PF00090; TSP\_1; 2.  
 DR Pfam; PF00791; ZU5; 1.  
 DR PRINTS; PRO1705; TSP1REPEAT.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00408; IGc2; 1.  
 DR SMART; SM00209; TSP1; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Apoptosis; Developmental protein; Immunoglobulin domain;  
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 30 Potential.  
 FT CHAIN 31 956 Netrin receptor UNC5D.  
 FT DOMAIN 31 382 Extracellular (Potential).  
 FT TRANSMEM 383 403 Potential.  
 FT DOMAIN 404 956 Cytoplasmic (Potential).  
 FT DOMAIN 52 149 Ig-like.  
 FT DOMAIN 151 242 Ig-like C2-type.  
 FT DOMAIN 250 304 TSP type-1 1.  
 FT DOMAIN 306 358 TSP type-1 2.  
 FT DOMAIN 543 645 ZU5.  
 FT DOMAIN 862 939 Death.  
 FT SITE 419 420 Cleavage (by caspase-3) (By similarity).  
 FT SITE 706 724 Interaction with DCC (By similarity).

FT DISULFID 73 132 By similarity.  
 FT DISULFID 178 229 By similarity.  
 FT CARBOHYD 115 115 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 226 226 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 351 351 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 379 379 N-linked (GlcNAc. . .) (Potential).  
 SQ SEQUENCE 956 AA; 106351 MW; DFDF07839C10C68D CRC64;  
  
 Query Match 43.9%; Score 245.5; DB 1; Length 956;  
 Best Local Similarity 46.2%; Pred. No. 1.le-17;  
 Matches 48; Conservative 21; Mismatches 34; Indels 1; Gaps 1;  
  
 Qy 1 TSNMTYGTNFNLGGRLMIPNTGISLLIPPAIPRGKIYIYLTLHKPEDVRLPLAGCQTL 60  
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 Db 543 TELRTTGVFGHLGGRLVMPNTGVSLLIPHGAYPEENSWEIYMSINQGEP-SLQSDGSEVL 601  
  
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPPDSWLSRLKKQSCEG 104  
 ||| |:|||| :||| | | : || : | : ||:: |||:: :|  
 Db 602 LSPEVTCGPPDMLVTPFALTIPHCADVSSEHNIHLKKRTQQG 645

RESULT 13  
 UN5D\_HUMAN  
 ID UN5D\_HUMAN STANDARD; PRT; 953 AA.  
 AC Q6UXZ4; Q8WYP7;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4)  
 DE (UNQ6012/PRO34692).  
 GN Name=UNC5D; Synonyms=KIAA1777, UNC5H4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RA Nakajima D., Nakayama M., Nagase T., Ohara O.;  
 RT "Identification of unc5H4 gene.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Receptor for netrin. May be involved in axon guidance by  
CC mediating axon repulsion of neuronal growth cones in the  
CC developing nervous system upon ligand binding. Axon repulsion in  
CC growth cones may be caused by its association with DCC that may  
CC trigger signaling for repulsion. It also acts as a dependence  
CC receptor required for apoptosis induction when not associated with  
CC netrin ligand (By similarity).  
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC       IsoId=Q6UXZ4-1; Sequence=Displayed;  
CC Name=2;  
CC       IsoId=Q6UXZ4-2; Sequence=VSP\_011703;  
CC       Note=No experimental confirmation available;  
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By  
CC similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleavage does not take place when the receptor is associated with  
CC netrin ligand. Its cleavage by caspases is required to induce  
CC apoptosis (By similarity).  
CC -!- SIMILARITY: Belongs to the UNC-5 family.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.  
CC -!- SIMILARITY: Contains 1 ZU5 domain.

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DR EMBL; AB055056; BAB83663.1; -.  
DR EMBL; AY358147; AAQ88514.1; -.  
DR HSSP; P07996; 1LSL.  
DR Genew; HGNC:18634; UNC5D.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH\_like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR008085; TSP\_1.  
DR InterPro; IPR000906; ZU5.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00047; ig; 1.  
DR Pfam; PF00090; TSP\_1; 2.  
DR Pfam; PF00791; ZU5; 1.  
DR PRINTS; PR01705; TSP1REPEAT.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00209; TSP1; 2.

DR PROSITE; PS50017; DEATH\_DOMAIN; FALSE\_NEG.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR PROSITE; PS50092; TSP1; 2.  
 KW Alternative splicing; Apoptosis; Developmental protein;  
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;  
 KW Transmembrane.  
 FT SIGNAL 1 32 Potential.  
 FT CHAIN 33 953 Netrin receptor UNC5D.  
 FT DOMAIN 33 379 Extracellular (Potential).  
 FT TRANSMEM 380 400 Potential.  
 FT DOMAIN 401 953 Cytoplasmic (Potential).  
 FT DOMAIN 54 151 Ig-like.  
 FT DOMAIN 153 244 Ig-like C2-type.  
 FT DOMAIN 252 306 TSP type-1 1.  
 FT DOMAIN 308 360 TSP type-1 2.  
 FT DOMAIN 540 642 ZU5.  
 FT DOMAIN 859 936 Death.  
 FT SITE 416 417 Cleavage (by caspase-3) (By similarity).  
 FT SITE 703 721 Interaction with DCC (By similarity).  
 FT DISULFID 75 134 By similarity.  
 FT DISULFID 180 231 By similarity.  
 FT CARBOHYD 117 117 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 228 228 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 353 353 N-linked (GlcNAc. . .) (Potential).  
 FT CARBOHYD 376 376 N-linked (GlcNAc. . .) (Potential).  
 FT VARSPLIC 1 34 MGRAAAATAGGGGGARRWLPWLGLCFWAAGTAAAR -> MIL  
 FT VLVKALSDVCAGTSGFLDFSSQTSP (in isoform  
 FT 2).  
 FT /FTId=VSP\_011703.  
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Query Match 43.6%; Score 243.5; DB 1; Length 953;  
 Best Local Similarity 45.2%; Pred. No. 1.8e-17;  
 Matches 47; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

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 | | | | | |||||:::||||| ||| :|||::::: | | | | : |  
 Db 540 TELRTTGVFGLGGRLVMPNTGVSSLIPHGAYPEENSWEIYMSINQGEP-SLQSDGSEVL 598  
 Qy 61 LSPIVSCGPPGVLLTRPVILAMDHCGEPSDWSLRKKQSCEG 104  
 ||| |:|||| ::::| | | : || : . | : ||:: |||:: :|  
 Db 599 LSPEVTCGPPDMIVTTPFALTIPHCADVSSEHNIHLKKRTQQG 642

#### RESULT 14

Q68DX9

ID Q68DX9 PRELIMINARY; PRT; 1267 AA.  
 AC Q68DX9;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZp686M05161.  
 GN Name=DKFZp686M05161;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Uterus endothel;  
RG The German cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DDJB databases.  
DR EMBL; CR749235; CAH18091.1; -.  
DR InterPro; IPR008144; Guanylate\_kin.  
DR InterPro; IPR008145; Guanyl/Ca.  
DR InterPro; IPR001478; PDZ.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR011511; SH3\_2.  
DR InterPro; IPR005417; ZonOcculdens.  
DR InterPro; IPR005418; ZonOcculS1.  
DR InterPro; IPR000906; ZU5.  
DR Pfam; PF00625; Guanylate\_kin; 1.  
DR Pfam; PF00595; PDZ; 1.  
DR Pfam; PF00018; SH3\_1; 1.  
DR Pfam; PF07653; SH3\_2; 1.  
DR Pfam; PF00791; ZU5; 1.  
DR PRINTS; PR01597; ZONOCLUDNS.  
DR PRINTS; PR01598; ZONOCLUDNS1.  
DR SMART; SM00072; GuKc; 1.  
DR SMART; SM00228; PDZ; 1.  
DR SMART; SM00218; ZU5; 1.  
DR PROSITE; PS50052; GUANYLATE\_KINASE\_2; 1.  
DR PROSITE; PS50106; PDZ; 1.  
DR PROSITE; PS50002; SH3; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 1267 AA; 142571 MW; 734B3877FBCAC6FA CRC64;

Query Match 34.3%; Score 192; DB 2; Length 1267;  
Best Local Similarity 43.6%; Pred. No. 1e-11;  
Matches 41; Conservative 12; Mismatches 39; Indels 2; Gaps 1;

QY 7 GTFNFLGGRLMIPNTGISLLIPDAIPRGKIEIYLTLHKPEDVRLPL--AGCQTLLSPI 64  
| || | | | ||:||:|| | || | | || : : : || :|||||:  
Db 1137 GIFNSNGGVLSIETGVSIIIPQGAIPEGVEQEIYFKVCRDNSILPPLDKEKGTLSSPL 1196  
  
QY 65 VSCGPPGVLLTRPVILAMDHCGEPSWDSLRK 98  
| || | | : :|| | : || :|| || ||  
Db 1197 VMCGPHGLKFLKPVELRLPHCASMTPDGWSFALK 1230

RESULT 15  
097758  
ID 097758 PRELIMINARY; PRT; 1769 AA.  
AC 097758;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ZO-1 MDCK.  
GN Name=ZO1-MDCK;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=breed: Cocker Spaniel;  
 RX MEDLINE=99196918; PubMed=10094817; DOI=10.1006/excr.1999.4392;  
 RA Gonzalez-Mariscal L., Islas S., Contreras R.G., Garcia-Villegas M.R.,  
 RA Betanzos A., Vega J., Diaz-Quinonez A., Martin-Orozco N.,  
 RA Ortiz-Navarrete V., Cereijido M., Valdes J.;  
 RT "Molecular characterization of the tight junction protein ZO-1 in MDCK  
 cells.";  
 RL Exp. Cell Res. 248:97-109(1999).  
 CC --!- SIMILARITY: Contains 3 PDZ/DHR domains.  
 DR EMBL; U55935; AAD11529.1; -.  
 DR HSSP; P31016; 1JXO.  
 DR GO; GO:0005923; C:tight junction; IEA.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR InterPro; IPR008144; Guanylate\_kin.  
 DR InterPro; IPR008145; Guanylt/Ca.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR011511; SH3\_2.  
 DR InterPro; IPR005417; ZonOcculdens.  
 DR InterPro; IPR005418; ZonOcculS1.  
 DR InterPro; IPR000906; ZU5.  
 DR Pfam; PF00625; Guanylate\_kin; 1.  
 DR Pfam; PF00595; PDZ; 3.  
 DR Pfam; PF07653; SH3\_2; 1.  
 DR Pfam; PF00791; ZU5; 1.  
 DR PRINTS; PRO1597; ZONOCLUDNS.  
 DR PRINTS; PRO1598; ZONOCLUDNS1.  
 DR SMART; SM00072; GuKc; 1.  
 DR SMART; SM00228; PDZ; 3.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00218; ZU5; 1.  
 DR PROSITE; PS50052; GUANYLATE\_KINASE\_2; 1.  
 DR PROSITE; PS50106; PDZ; 3.  
 DR PROSITE; PS50002; SH3; 1.  
 SQ SEQUENCE 1769 AA; 197606 MW; 181E9F36CEBC96EF CRC64;

Query Match 34.3%; Score 192; DB 2; Length 1769;  
 Best Local Similarity 43.6%; Pred. No. 1.5e-11;  
 Matches 41; Conservative 12; Mismatches 39; Indels 2; Gaps 1;

Qy	7 GTFNFLGGRLMIPNTGISLLIPPDAlPRGKIYEIYLTLHKPEDVRLPL--AGCQTLLSPI 64
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Db	1639 GVFNNNGGVLSIETGVSIIIPQGAIPPEGVEQEIYFKVCRDNSILPPLDKEKGTLSSPL 1698
Qy	65 VSCGPPGVLLTRPVILAMDHCGEPSDWSLRK 98
	: :      :    :
Db	1699 VMCGPHGLKFLKPVELRLPHCASMPDGWSFALK 1732

Search completed: March 1, 2005, 09:03:41  
 Job time : 21.025 secs